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Tami M. Procopio
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Aya Jakobovits, et al.

Serial No.: 10/001,469

Filing Date: October 31, 2001

For: NUCLEIC ACID AND CORRESPONDING
PROTEINS ENTITLED 101P3A11
USEFUL IN TREATMENT AND
DETECTION OF CANCER

Examiner: To be Assigned

Group Art Unit: 1642

AMENDMENT

Box Missing Parts
Assistant Commissioner For Patents
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to file missing parts of non-provisional application mailed December 20, 2001, for which a response is due on February 20, 2002. A petition for an extension of time of three (3) months until 20 May 2002 is attached hereto, along with the required fee.

Please enter the following sequence listing, amendments and remarks.

In the Specification

On page 1, line 26, please insert new paragraph as follows:

--SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (COPY 1) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a duplicate compact disc copy of Sequence Listing (COPY 2) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a computer readable form copy of the Sequence Listing (CRF COPY) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB).--

In the Sequence Listing

Please insert the attached compact disc copy of the Sequence Listing on CD-R (COPY 1) in the above-captioned application. A duplicate compact disc copy of the Sequence Listing on CD-R (COPY 2) and a computer readable form copy of the Sequence Listing on CD-R (CRF COPY) accompany this response.

AMENDMENTS

In the Specification:

Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph:

-- **Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960).** The 101P3A11 SSH sequence.--

Please replace the paragraph beginning at page 7, line 22, with the following rewritten paragraph:

-- **Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11.** The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).--

Please replace the paragraph beginning at page 7, line 26, with the following rewritten paragraph:

--**Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962).** The 101P3A11 protein has 317 amino acids.--

Please replace the paragraph beginning at page 7, line 28, with the following rewritten paragraph:

--**Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963)** The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25) predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.--

Please replace the paragraph beginning at page 11, line 31, with the following rewritten paragraph:

--**Figure 23.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 1, with the following rewritten paragraph:

--**Figure 24.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 3, with the following rewritten paragraph:

--**Figure 25.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).--

Please replace the paragraph beginning at page 36, line 20, with the following rewritten paragraph:

--Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.--

Please replace the paragraph beginning at page 70, line 3, with the following rewritten paragraph:

--In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.--

Please replace the paragraph beginning at page 70, line 11, with the following rewritten paragraph:

--Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-

binding epitope peptide having the formula: aKXVAAWTLKAAa (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.--

Please replace the paragraph beginning at page 80, line 16, with the following rewritten paragraph:

--Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.--

Please replace the paragraph beginning at page 86, line 29, with the following rewritten paragraph:

--pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-

terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScissionTM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 8, with the following rewritten paragraph:

--pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 20, with the following rewritten paragraph:

--**pET Constructs:** To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag TM that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.--

Please replace the paragraph beginning at page 88, line 19, with the following rewritten paragraph:

--**pcDNA4/HisMax Constructs:** To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has XpressTM and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*--

Please replace the paragraph beginning at page 88, line 28, with the following rewritten paragraph:

--**pcDNA3.1/MycHis Constructs:** To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 16, with the following rewritten paragraph:

--**PAPtag:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 27, with the following rewritten paragraph:

--**ptag5:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for

selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*--

Please replace the paragraph beginning at page 90, line 30, with the following rewritten paragraph:

--Additional pSR α constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSR α constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.--

Please replace the paragraph beginning at page 141, line 31, with the following rewritten paragraph:

--The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in 293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.--

Please replace Table XIX, beginning at page 186, with the following rewritten Table XIX:

--Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site



Number of matches: 3

- 1 7-10 NESS (SEQ ID NO: 1410)
- 2 44-47 NLTI (SEQ ID NO: 1411)
- 3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site

Number of matches: 3

- 1 56-59 SLHE (SEQ ID NO: 1414)
- 2 69-72 SGID (SEQ ID NO: 1415)
- 3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 1 6-11 GNESSA (SEQ ID NO: 1417)
- 2 21-26 GLEEAQ (SEQ ID NO: 1418)
- 3 111-116 GMESTV (SEQ ID NO: 1419)
- 4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature

112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)--

Please replace Table XXI, beginning at page 190, line 1, with the following rewritten

Table XXI:

--Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

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1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN
361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCAA NNCNGGTACT
541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGNAA AAGGGGNAAN
661 CGGGGCGAAA TGNNAAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA

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781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG--

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Please replace Table XXII, beginning at page 190, line 38, with the following rewritten

Table XXII:

--Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89

Identities = 215/223 (96%), Gaps = 6/223 (2%)

Strand = Plus / Plus

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101P3A11: 68  cacattccttccatacgggttgagcctctacctgcctggtgctggtcacagttcagcttct 127
(SEQ ID NO: 1423)
Variant : 1  cacattccttccatacgggttgagcctctacctgcctggtgctggtcacagttcagcttct 60
(SEQ ID NO: 1424)

101P3A11: 128  tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcatecctaataaggcc 187
Variant : 61  tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcatecctaataaggcc 120

101P3A11: 188  tccctggtttagaagaggctcagttctggttgcccttccattgtgtctcctctacctta 247
Variant : 121  tccctggtttagaagaggctcagttctggttgcc--tccattgtgtctcctctanct-- 177

101P3A11: 248  ttgctgtgctaggttaacttgacaatcatctacattgtgcgga 290
Variant : 178  atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcgga 217--

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Please replace Table XXIII, beginning at page 191, line 8, with the following rewritten

Table XXIII:

--Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect (2) = 3e-29

Identities = 51/51 (100%)

Frame = +1 / +3

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101P3A11: 70  HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
(SEQ ID NO: 1425)
Variant : 3  HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
(SEQ ID NO: 1426)--

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Please replace Table XXIV, beginning at page 191, line 16, with the following rewritten

Table XXIV:

--Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWRXGVMXPRVXECLAKTSIMXTXYNGXESXXRKAKEXPXXGT LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPDRDGKRGXRGEKXTGXRGXKXGXXEG XGSREKXNXGXETXXXARXXKEXXXXXKSKSXGXKXGGXXXPXXXKXXXGXTRKXXG XXGK*XGNXXANRTXGKTGTGXAXRXXXPEXR
Frame 2 (SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTQQLLDGGSQWQ*IQCYILHPNRPWFRRGSVLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAVHVPWQQDRAGTNGGEXG*RTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PKXXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXXKXGXGAKXXKPGPGEXXRGXXVKD XVQGXKTXGXKPFXXPGXERXXXXXKXKAXAXKXGEXKXGRXKTXGXXHGXXXA XKGNXXGTXQTXRXERNPPEXXNAXXXPSXG
Frame 3 (SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTPIXLSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHXXNV*RRRIGXAQG*GXXQXXYF NPAXGXXTGXXNKEGXXLGQNGXGXXRTHGXKGRXKXGXGRNXXNRXPGXXEGEXX*RT GFGKXKPKXXRNXXSGPGXKXGXGKIXKXKXKXGXXXTXXXKXKXGXXTEXXGR XREIXREXKXKPKXGRNETHRXRXTXXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*) indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.--

Please replace Table XXVI, beginning at page 193, line 1, with the following rewritten

Table XXVI:

--Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

<u>HLA-A1 nonomers</u>											
	Pos	1	2	3	4	5	6	7	8	9	score
1	245	H	V	C	A	V	F	I	F	Y	24
2	29	L	A	F	P	L	C	S	L	Y	21
3	41	V	L	G	N	L	T	I	I	Y	21
4	285	P	P	V	L	N	P	I	V	Y	20
5	111	G	M	E	S	T	V	L	L	A	19
6	117	L	L	A	M	A	F	D	R	Y	19
7	172	R	S	N	I	L	S	H	S	Y	19
8	192	D	D	I	R	V	N	V	V	Y	19
9	212	D	S	L	L	I	S	F	S	Y	19
10	57	L	H	E	P	M	Y	I	F	L	18
11	22	L	E	E	A	Q	F	W	L	A	17
12	9	S	S	A	T	Y	F	I	L	I	16
13	52	R	T	E	H	S	L	H	E	P	16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score	
14	54	E	<u>H</u>	S	L	H	E	<u>P</u>	M	Y	16	
15	78	S	<u>S</u>	M	P	K	M	<u>L</u>	A	I	16	
16	95	Q	<u>F</u>	D	A	C	L	<u>L</u>	Q	I	16	
17	159	A	<u>P</u>	L	P	V	F	<u>I</u>	K	Q	16	
18	183	H	<u>Q</u>	D	V	M	K	<u>L</u>	A	C	16	
19	1	M	<u>V</u>	D	P	N	G	<u>N</u>	E	S	15	
20	5	N	<u>G</u>	D	E	S	S	<u>A</u>	T	Y	15	
21	210	G	<u>L</u>	N	D	S	L	L	I	S	F	15
22	273	L	<u>P</u>	V	I	L	A	<u>N</u>	I	Y	15	
23	271	S	<u>P</u>	L	P	V	I	<u>L</u>	A	N	14	
24	91	S	<u>T</u>	T	I	Q	F	<u>D</u>	A	C	13	
25	121	A	<u>F</u>	D	R	Y	V	<u>A</u>	I	C	13	
26	138	L	<u>T</u>	L	P	R	V	<u>T</u>	K	I	13	
27	218	F	<u>S</u>	Y	L	L	I	<u>L</u>	K	T	13	
28	282	L	<u>L</u>	V	P	P	V	<u>L</u>	N	P	13	
29	190	A	<u>C</u>	D	D	I	R	<u>V</u>	N	V	12	
30	191	C	<u>D</u>	D	I	R	V	<u>N</u>	K	V	12	
31	231	T	<u>R</u>	E	A	Q	A	<u>K</u>	A	F	12	
32	268	R	<u>R</u>	D	S	P	L	<u>P</u>	V	I	12	
33	270	D	S	<u>P</u>	L	P	V	I	L	A	12	

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	L	N	P	I	<u>V</u>	Y	G	V	30
2	14	F	I	L	I	G	<u>L</u>	P	G	L	29
3	28	W	L	A	F	P	<u>L</u>	C	S	L	28
4	37	Y	L	I	A	V	<u>L</u>	G	N	L	28
5	222	L	I	L	K	T	<u>V</u>	L	G	L	28
6	66	C	M	L	S	G	<u>I</u>	D	I	L	26
7	108	S	L	S	G	M	<u>E</u>	S	T	V	26
8	181	C	L	H	Q	D	<u>V</u>	M	K	L	26
9	201	G	L	I	V	I	<u>I</u>	S	A	I	26
10	214	L	L	I	S	F	<u>S</u>	Y	L	L	26
11	275	V	I	L	A	N	<u>I</u>	Y	L	L	26
12	157	L	M	A	P	L	<u>P</u>	V	F	I	25
13	220	Y	L	L	I	L	<u>K</u>	T	V	L	25
14	276	I	L	A	N	I	<u>Y</u>	L	L	V	25
15	279	N	I	Y	L	L	<u>V</u>	P	P	V	25
16	138	L	T	L	P	R	<u>V</u>	T	K	I	24
17	213	S	L	L	I	S	<u>F</u>	S	Y	L	24
18	49	Y	I	V	R	T	<u>E</u>	H	S	L	23
19	143	V	T	K	I	G	<u>V</u>	A	A	V	23
20	188	K	L	A	C	D	<u>D</u>	I	R	V	23
21	198	V	V	Y	G	L	<u>I</u>	V	I	I	23
22	21	G	L	E	E	A	<u>Q</u>	F	W	L	22
23	40	A	V	L	G	N	<u>L</u>	T	I	I	22
24	206	I	S	A	I	G	<u>L</u>	D	S	L	22
25	11	A	T	Y	F	I	<u>L</u>	I	G	L	21
26	60	P	M	Y	I	F	<u>L</u>	C	M	L	21

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
27	135	A T V L T <u>L</u> P R V	21
28	160	P L P V F <u>I</u> K Q L	21
29	174	N I L S H <u>S</u> Y C L	21
30	207	S A I G L <u>D</u> S L L	21
31	272	P L P V I <u>L</u> A N I	21
32	283	L V P P V <u>L</u> N P I	21
33	67	M L S G I <u>D</u> I L I	20
34	101	L Q I F A <u>I</u> H S L	20
35	282	L L V P P V <u>L</u> N P	20
36	299	E I R Q R <u>I</u> L R L	20
37	304	I L R L F <u>H</u> V A T	20
38	39	I A V L G <u>N</u> L T I	19
39	45	L T I I Y <u>I</u> V R T	19
40	92	T T I Q F <u>D</u> A C L	19
41	110	S G M E S <u>T</u> V L L	19
42	127	A I C H P <u>L</u> R H A	19
43	132	L R H A T <u>V</u> L T L	19
44	149	A A V V R <u>G</u> A A L	19
45	155	A A L M A <u>P</u> L P V	19
46	156	A L M A P <u>L</u> P V F	19
47	203	I V I I S <u>A</u> I G L	19
48	208	A I G L D <u>S</u> L L I	19
49	216	I S F S Y <u>L</u> L I L	19
50	219	S Y L L I <u>L</u> K T V	19
51	221	L L I L K <u>T</u> V L G	19
52	223	I L K T V <u>L</u> G L T	19
53	17	I G L P G <u>L</u> E E A	18
54	33	L C S L Y <u>L</u> I A V	18
55	34	C S L Y L <u>I</u> A V L	18
56	38	L I A V L <u>G</u> N L T	18
57	43	G N L T I <u>I</u> Y I V	18
58	85	A I F W F <u>N</u> S T T	18
59	118	L A M A F <u>D</u> R Y V	18
60	194	I R V N V <u>V</u> Y G L	18
61	210	G L D S L <u>L</u> I S F	18
62	215	L I S F S <u>Y</u> L L I	18
63	246	V C A V F <u>I</u> F Y V	18
64	254	V P F I G <u>L</u> S M V	18
65	15	I L I G L <u>P</u> G L E	17
66	63	I F L C M <u>L</u> S G I	17
67	72	D I L I S <u>T</u> S S M	17
68	93	T I Q F D <u>A</u> C L L	17
69	98	A C L L Q <u>I</u> F A I	17
70	111	G M E S T <u>V</u> L L A	17
71	120	M A F D R <u>Y</u> V A I	17
72	167	Q L P F C <u>R</u> S N I	17
73	197	N V V Y G <u>L</u> I V I	17
74	226	T V L G L <u>T</u> R E A	17
75	281	Y L L V P <u>P</u> V L N	17

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
76	31	F	P	L	C	S	<u>L</u>	Y	L	I	16
77	56	S	L	H	E	P	<u>M</u>	Y	I	F	16
78	70	G	I	D	I	L	<u>I</u>	S	T	S	16
79	78	S	S	M	P	K	<u>M</u>	L	A	I	16
80	79	S	M	P	K	M	<u>L</u>	A	I	F	16
81	104	F	A	I	H	S	<u>L</u>	S	G	M	16
82	119	A	M	A	F	D	<u>R</u>	Y	V	A	16
83	144	T	K	I	G	V	<u>A</u>	A	V	V	16
84	147	G	V	A	A	V	<u>V</u>	R	G	A	16
85	186	V	M	K	L	A	<u>C</u>	D	D	I	16
86	230	L	T	R	E	A	<u>Q</u>	A	K	A	16
87	238	A	F	G	T	C	<u>V</u>	S	H	V	16
88	249	V	F	I	F	Y	<u>V</u>	P	F	I	16
89	302	Q	R	I	L	R	<u>L</u>	F	H	V	16
90	303	R	I	L	R	L	<u>F</u>	H	V	A	16
91	18	G	L	P	G	L	<u>E</u>	E	A	Q	15
92	35	S	L	Y	L	I	<u>A</u>	V	L	G	15
93	42	L	G	N	L	T	<u>I</u>	I	Y	I	15
94	46	T	I	I	Y	I	<u>V</u>	R	T	E	15
95	69	S	G	I	D	I	<u>L</u>	I	S	T	15
96	76	S	T	S	S	M	<u>P</u>	K	M	L	15
97	131	P	L	R	H	A	<u>T</u>	V	L	T	15
98	137	V	L	T	L	P	<u>R</u>	V	T	K	15
99	153	R	G	A	A	L	<u>M</u>	A	P	L	15
100	190	A	C	D	D	I	<u>R</u>	V	N	V	15
101	191	C	D	D	I	R	<u>V</u>	N	V	V	15
102	204	V	I	I	S	A	<u>I</u>	G	L	D	15
103	241	T	C	V	S	H	<u>V</u>	C	A	V	15
104	251	I	F	Y	V	P	<u>F</u>	I	G	L	15
105	269	R	D	S	P	L	<u>P</u>	V	I	L	15
106	280	I	Y	L	L	V	<u>P</u>	P	V	L	15
107	306	R	L	F	H	V	<u>A</u>	T	H	A	15

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	148	V	<u>A</u>	A	V	V	R	G	A	A	14
2	119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	13
3	147	G	<u>V</u>	A	A	V	V	R	G	A	12
4	97	D	<u>A</u>	C	L	L	Q	<u>I</u>	F	A	11
5	127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	10
6	3	D	<u>P</u>	N	G	N	E	<u>S</u>	S	A	9
7	17	I	<u>G</u>	L	P	G	L	<u>E</u>	E	A	9
8	22	L	<u>E</u>	E	A	Q	F	<u>W</u>	L	A	9
9	32	P	<u>L</u>	C	S	L	Y	<u>L</u>	I	A	9
10	77	T	<u>S</u>	S	M	P	K	<u>M</u>	L	A	9
11	90	N	<u>S</u>	T	T	I	Q	<u>F</u>	D	A	9

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
12	111	G	<u>M</u>	E	S	T	V	<u>L</u>	L	A	9
13	113	E	<u>S</u>	T	V	L	L	<u>A</u>	M	A	9
14	141	P	<u>R</u>	V	T	K	I	<u>G</u>	V	A	9
15	142	R	<u>V</u>	T	K	I	G	<u>V</u>	A	A	9
16	151	V	<u>V</u>	R	G	A	A	<u>L</u>	M	A	9
17	182	L	<u>H</u>	Q	D	V	M	<u>K</u>	L	A	9
18	200	Y	<u>G</u>	L	I	V	I	<u>I</u>	S	A	9
19	226	T	<u>V</u>	L	G	L	T	<u>R</u>	E	A	9
20	228	L	<u>G</u>	L	T	R	E	<u>A</u>	Q	A	9
21	230	L	<u>T</u>	R	E	A	Q	<u>A</u>	K	A	9
22	240	G	<u>T</u>	C	V	S	H	<u>V</u>	C	A	9
23	270	D	<u>S</u>	P	L	P	V	<u>I</u>	L	A	9
24	303	R	<u>I</u>	L	R	L	F	<u>H</u>	V	A	9
25	306	R	<u>L</u>	F	H	V	A	<u>T</u>	H	A	9

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
30	150	A V V R G A A L M	19
31	174	N I L S H S Y C L	19
32	192	D D I R V N V V Y	19
33	214	L L I S F S Y L L	19
34	251	I F Y V P F I G L	19
35	8	E S S A T Y F I L	18
36	21	G L E E A Q F W L	18
37	45	L T I I Y I V R T	18
38	54	E H S L H E P M Y	18
39	59	E P M Y I F L C M	18
40	88	W F N S T T I Q F	18
41	93	T I Q F D A C L L	18
42	185	D V M K L A C D D	18
43	198	V V Y G L I V I I	18
44	62	Y I F L C M L S G	17
45	70	G I D I L I S T S	17
46	79	S M P K M L A I F	17
47	96	F D A C L L Q I F	17
48	104	F A I H S L S G M	17
49	138	L T L P R V T K I	17
50	143	V T K I G V A A V	17
51	204	V I I S A I G L D	17
52	212	D S L L I S F S Y	17
53	220	Y L L I L K T V L	17
54	256	F I G L S M V H R	17
55	283	L V P P V L N P I	17
56	29	L A F P L C S L Y	16
57	40	A V L G N L T I I	16
58	46	T I I Y I V R T E	16
59	52	R T E H S L H E P	16
60	75	I S T S S M P K M	16
61	91	S T T I Q F D A C	16
62	135	A T V L T L P R V	16
63	147	G V A A V V R G A	16
64	201	G L I V I I S A I	16
65	257	I G L S M V H R F	16
66	279	N I Y L L V P P V	16
67	30	A F P L C S L Y L	15
68	101	L Q I F A I H S L	15
69	115	T V L L A M A F D	15
70	127	A I C H P L R H A	15
71	153	R G A A L M A P L	15
72	163	V F I K Q L P F C	15
73	215	L I S F S Y L L I	15
74	216	I S F S Y L L I L	15
75	225	K T V L G L T R E	15
76	272	P L P V I L A N I	15
77	282	L L V P P V L N P	15
78	286	P V L N P I V Y G	15

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
79	287	V	L	N	P	I	V	Y	G	V	15
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	L	T	L	P	R	V	T	K	30
2	229	G	L	T	R	E	A	Q	A	K	27
3	145	K	I	G	V	A	A	V	V	R	26
4	150	A	V	V	R	G	A	A	L	M	24
5	290	P	I	V	Y	G	V	K	T	K	24
6	35	S	L	Y	L	I	A	V	L	G	23
7	156	A	L	M	A	P	L	P	V	F	23
8	47	I	I	Y	I	V	R	T	E	H	22
9	50	I	V	R	T	E	H	S	L	H	22
10	142	R	V	T	K	I	G	V	A	A	22
11	151	V	V	R	G	A	A	L	M	A	22
12	242	C	V	S	H	V	C	A	V	F	22
13	248	A	V	F	I	F	Y	V	P	F	22
14	116	V	L	L	A	M	A	F	D	R	21
15	192	D	D	I	R	V	N	V	V	Y	21
16	303	R	I	L	R	L	F	H	V	A	21
17	304	I	L	R	L	F	H	V	A	T	21
18	108	S	L	S	G	M	E	S	T	V	20
19	198	V	V	Y	G	L	I	V	I	I	20
20	291	I	V	Y	G	V	K	T	K	E	20
21	15	I	L	I	G	L	P	G	L	E	19
22	44	N	L	T	I	I	Y	I	V	R	19
23	73	I	L	I	S	T	S	S	M	P	19
24	74	L	I	S	T	S	S	M	P	K	19
25	99	C	L	L	Q	I	F	A	I	H	19
26	162	P	V	F	I	K	Q	L	P	F	19
27	203	I	V	I	I	S	A	I	G	L	19
28	221	L	L	I	L	K	T	V	L	G	19
29	245	H	V	C	A	V	F	I	F	Y	19
30	306	R	L	F	H	V	A	T	H	A	19
31	40	A	V	L	G	N	L	T	I	I	18
32	85	A	I	F	W	F	N	S	T	T	18
33	205	I	I	S	A	I	G	L	D	S	18
34	220	Y	L	L	I	L	K	T	V	L	18
35	253	Y	V	P	F	I	G	L	S	M	18
36	37	Y	L	I	A	V	L	G	N	L	17
37	41	V	L	G	N	L	T	I	I	Y	17
38	117	L	L	A	M	A	F	D	R	Y	17
39	131	P	L	R	H	A	T	V	L	T	17
40	136	T	V	L	T	L	P	R	V	T	17

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
41	180	Y	C	<u>L</u>	H	Q	<u>D</u>	<u>V</u>	M	K	17
42	201	G	<u>L</u>	<u>I</u>	V	I	<u>I</u>	<u>S</u>	A	I	17
43	213	S	<u>L</u>	<u>L</u>	I	S	<u>F</u>	<u>S</u>	Y	L	17
44	256	F	I	<u>G</u>	<u>L</u>	S	<u>M</u>	<u>V</u>	H	R	17
45	261	M	<u>V</u>	<u>H</u>	R	F	<u>S</u>	<u>K</u>	R	R	17
46	276	I	<u>L</u>	<u>A</u>	N	I	<u>Y</u>	<u>L</u>	L	V	17
47	281	Y	<u>L</u>	<u>L</u>	V	P	<u>P</u>	<u>V</u>	L	N	17
48	286	P	<u>V</u>	<u>L</u>	N	P	<u>I</u>	<u>V</u>	Y	G	17
49	288	L	N	<u>P</u>	I	V	<u>Y</u>	<u>G</u>	V	K	17
50	309	H	<u>V</u>	<u>A</u>	T	H	<u>A</u>	<u>S</u>	E	P	17
51	1	M	<u>V</u>	<u>D</u>	P	N	<u>G</u>	<u>N</u>	E	S	16
52	56	S	<u>L</u>	<u>H</u>	E	P	<u>M</u>	<u>Y</u>	I	F	16
53	70	G	<u>I</u>	<u>D</u>	I	L	<u>I</u>	<u>S</u>	T	S	16
54	72	D	<u>I</u>	<u>L</u>	I	S	<u>T</u>	<u>S</u>	S	M	16
55	115	T	<u>V</u>	<u>L</u>	L	A	<u>M</u>	<u>A</u>	F	D	16
56	125	Y	<u>V</u>	<u>A</u>	I	C	<u>H</u>	<u>P</u>	L	R	16
57	144	T	<u>K</u>	<u>I</u>	<u>G</u>	V	<u>A</u>	<u>A</u>	V	V	16
58	167	Q	<u>L</u>	<u>P</u>	F	C	<u>R</u>	<u>S</u>	N	I	16
59	175	I	<u>L</u>	<u>S</u>	H	S	<u>Y</u>	<u>C</u>	L	H	16
60	195	R	<u>V</u>	<u>N</u>	V	V	<u>Y</u>	<u>G</u>	L	I	16
61	197	N	<u>V</u>	<u>V</u>	Y	<u>G</u>	<u>L</u>	<u>I</u>	V	I	16
62	210	G	<u>L</u>	<u>D</u>	S	L	<u>L</u>	<u>I</u>	S	F	16
63	282	L	<u>L</u>	<u>V</u>	P	P	<u>V</u>	<u>L</u>	N	P	16
64	299	E	<u>I</u>	<u>R</u>	Q	R	<u>I</u>	<u>L</u>	R	L	16
65	301	R	<u>Q</u>	<u>R</u>	I	L	<u>R</u>	<u>L</u>	F	H	16
66	16	L	<u>I</u>	<u>G</u>	L	P	<u>G</u>	<u>L</u>	E	E	15
67	46	T	<u>I</u>	<u>I</u>	Y	I	<u>V</u>	<u>R</u>	T	E	15
68	102	Q	<u>I</u>	<u>F</u>	A	I	<u>H</u>	<u>S</u>	L	S	15
69	193	D	<u>I</u>	<u>R</u>	V	N	<u>V</u>	<u>V</u>	Y	G	15
70	208	A	<u>I</u>	<u>G</u>	L	D	<u>S</u>	<u>L</u>	L	I	15
71	223	I	<u>L</u>	<u>K</u>	T	V	<u>L</u>	<u>G</u>	L	T	15
72	237	K	<u>A</u>	<u>F</u>	G	T	<u>C</u>	<u>V</u>	S	H	15

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	P	L	R	H	A	T	V	L	22
2	59	E	P	M	Y	I	F	L	C	M	21
3	168	L	P	F	C	R	S	N	I	L	20
4	289	N	P	I	V	Y	G	V	K	T	19
5	3	D	P	N	G	N	E	S	S	A	18
6	19	L	P	G	L	E	E	A	Q	F	18
7	140	L	P	R	V	T	K	I	G	V	18
8	284	V	P	P	V	L	N	P	I	V	17
9	31	F	P	L	C	S	L	Y	L	I	16
10	254	V	P	F	I	G	L	S	M	V	16
11	269	R	D	S	P	L	P	V	I	L	16

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
12	149	A A V V R G A A L	15
13	153	R G A A L M A P L	15
14	156	A L M A P L P V F	15
15	251	I F Y V P F I G L	15
16	299	E I R Q R I L R L	15
17	8	E S S A T Y F I L	14
18	28	W L A F P L C S L	14
19	30	A F P L C S L Y L	14
20	110	S G M E S T V L L	14
21	132	L R H A T V L T L	14
22	159	A P L P V F I K Q	14
23	222	L I L K T V L G L	14
24	271	S P L P V I L A N	14
25	25	A Q F W L A F P L	13
26	109	L S G M E S T V L	13
27	124	R Y V A I C H P L	13
28	216	I S F S Y L L I L	13
29	268	R R D S P L P V I	13
30	280	I Y L L V P P V L	13
31	11	A T Y F I L I G L	12
32	34	C S L Y L I A V L	12
33	57	L H E P M Y I F L	12
34	76	S T S S M P K M L	12
35	142	R V T K I G V A A	12
36	151	V V R G A A L M A	12
37	190	A C D D I R V N V	12
38	194	I R V N V V Y G L	12
39	206	I S A I G L D S L	12
40	207	S A I G L D S L L	12
41	220	Y L L I L K T V L	12
42	267	K R R D S P L P V	12
43	304	I L R L F H V A T	12
44	14	F I L I G L P G L	11
45	23	E E A Q F W L A F	11
46	37	Y L I A V L G N L	11
47	40	A V L G N L T I I	11
48	77	T S S M P K M L A	11
49	78	S S M P K M L A I	11
50	80	M P K M L A I F W	11
51	92	T T I Q F D A C L	11
52	112	M E S T V L L A M	11
53	119	A M A F D R Y V A	11
54	127	A I C H P L R H A	11
55	131	P L R H A T V L T	11
56	155	A A L M A P L P V	11
57	157	L M A P L P V F I	11
58	181	C L H Q D V M K L	11
59	203	I V I I S A I G L	11
60	208	A I G L D S L L I	11

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
61	213	S L L I S F S Y L	11
62	248	A V F I F Y V P F	11
63	265	F S K R R D S P L	11
64	275	V I L A N I Y L L	11
65	285	P P V L N P I V Y	11

HLA-B*08 nonomers (SEQ ID
NOS 1813-1847, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	299	E I R Q R I L R L	31
2	265	F S K R R D S P L	29
3	149	A A V V R G A A L	24
4	168	L P F C R S N I L	24
5	294	G V K T K E I R Q	21
6	120	M A F D R Y V A I	20
7	292	V Y G V K T K E I	20
8	21	G L E E A Q F W L	19
9	78	S S M P K M L A I	19
10	160	P L P V F I K Q L	19
11	186	V M K L A C D D I	18
12	213	S L L I S F S Y L	18
13	221	L L I L K T V L G	18
14	296	K T K E I R Q R I	18
15	297	T K E I R Q R I L	18
16	130	H P L R H A T V L	17
17	181	C L H Q D V M K L	17
18	223	I L K T V L G L T	17
19	28	W L A F P L C S L	16
20	37	Y L I A V L G N L	16
21	56	S L H E P M Y I F	16
22	80	M P K M L A I F W	16
23	162	P V F I K Q L P F	16
24	201	G L I V I I S A I	16
25	207	S A I G L D S L L	16
26	214	L L I S F S Y L L	16
27	220	Y L L I L K T V L	16
28	233	E A Q A K A F G T	16
29	275	V I L A N I Y L L	16
30	304	I L R L F H V A T	16
31	14	F I L I G L P G L	15
32	110	S G M E S T V L L	15
33	138	L T L P R V T K I	15
34	164	F I K Q L P F C R	15
35	222	L I L K T V L G L	15

HLA-B*1510 nonomers (SEQ ID
NOS 1848-1890, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	score
1 57	L	H	E	P	M	Y	I	F	L	23
2 244	S	H	V	C	A	V	F	I	F	17
3 269	R	D	S	P	L	P	V	I	L	16
4 280	I	Y	L	L	V	P	P	V	L	16
5 262	V	H	R	F	S	K	R	R	D	15
6 299	E	I	R	Q	R	I	L	R	L	15
7 106	I	H	S	L	S	G	M	E	S	14
8 206	I	S	A	I	G	L	D	S	L	14
9 220	Y	L	L	I	L	K	T	V	L	14
10 251	I	F	Y	V	P	F	I	G	L	14
11 297	T	K	E	I	R	Q	R	I	L	14
12 21	G	L	E	E	A	Q	F	W	L	13
13 34	C	S	L	Y	L	I	A	V	L	13
14 54	E	H	S	L	H	E	P	M	Y	13
15 110	S	G	M	E	S	T	V	L	L	13
16 194	I	R	V	N	V	V	Y	G	L	13
17 8	E	S	S	A	T	Y	F	I	L	12
18 14	F	I	L	I	G	L	P	G	L	12
19 28	W	L	A	F	P	L	C	S	L	12
20 66	C	M	L	S	G	I	D	I	L	12
21 76	S	T	S	S	M	P	K	M	L	12
22 92	T	T	I	Q	F	D	A	C	L	12
23 109	L	S	G	M	E	S	T	V	L	12
24 130	H	P	L	R	H	A	T	V	L	12
25 132	L	R	H	A	T	V	L	T	L	12
26 149	A	A	V	V	R	G	A	A	L	12
27 153	R	G	A	A	L	M	A	P	L	12
28 160	P	L	P	V	F	I	K	Q	L	12
29 181	C	L	H	Q	D	V	M	K	L	12
30 182	L	H	Q	D	V	M	K	L	A	12
31 203	I	V	I	I	S	A	I	G	L	12
32 216	I	S	F	S	Y	L	L	I	L	12
33 222	L	I	L	K	T	V	L	G	L	12
34 275	V	I	L	A	N	I	Y	L	L	12
35 37	Y	L	I	A	V	L	G	N	L	11
36 49	Y	I	V	R	T	E	H	S	L	11
37 93	T	I	Q	F	D	A	C	L	L	11
38 101	L	Q	I	F	A	I	H	S	L	11
39 129	C	H	P	L	R	H	A	T	V	11
40 133	R	H	A	T	V	L	T	L	P	11
41 177	S	H	S	Y	C	L	H	Q	D	11
42 207	S	A	I	G	L	D	S	L	L	11
43 257	I	G	L	S	M	V	H	R	F	11

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	score
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sd-79244

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HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos		1	2	3	4	5	6	7	8	9	score
1	194		I	R	V	N	V	V	Y	G	L	25
2	268		R	R	D	S	P	L	P	V	I	24
3	132		L	R	H	A	T	V	L	T	L	23
4	300		I	R	Q	R	I	L	R	L	F	23
5	305		L	R	L	F	H	V	A	T	H	23
6	231		T	R	E	A	Q	A	K	A	F	21
7	34		C	S	L	Y	L	I	A	V	L	18
8	299		E	I	R	Q	R	I	L	R	L	18
9	6		G	N	E	S	S	A	T	Y	F	17
10	66		C	M	L	S	G	I	D	I	L	17
11	162		P	V	F	I	K	Q	L	P	F	17
12	207		S	A	I	G	L	D	S	L	L	17
13	210		G	L	D	S	L	L	I	S	F	17
14	220		Y	L	L	I	L	K	T	V	L	17
15	237		K	A	F	G	T	C	V	S	H	17
16	269		R	D	S	P	L	P	V	I	L	17
17	280		I	Y	L	L	V	P	P	V	L	17
18	295		V	K	T	K	E	I	R	Q	R	17
19	11		A	T	Y	F	I	L	I	G	L	16
20	14		F	I	L	I	G	L	P	G	L	16
21	21		G	L	E	E	A	Q	F	W	L	16
22	25		A	Q	F	W	L	A	F	P	L	16
23	37		Y	L	I	A	V	L	G	N	L	16
24	92		T	T	I	Q	F	D	A	C	L	16
25	101		L	Q	I	F	A	I	H	S	L	16
26	124		R	Y	V	A	I	C	H	P	L	16
27	130		H	P	L	R	H	A	T	V	L	16
28	141		P	R	V	T	K	I	G	V	A	16
29	153		R	G	A	A	L	M	A	P	L	16
30	181		C	L	H	Q	D	V	M	K	L	16
31	201		G	L	I	V	I	I	S	A	I	16
32	203		I	V	I	I	S	A	I	G	L	16
33	216		I	S	F	S	Y	L	L	I	L	16
34	222		L	I	L	K	T	V	L	G	L	16
35	255		P	F	I	G	L	S	M	V	H	16
36	257		I	G	L	S	M	V	H	R	F	16
37	275		V	I	L	A	N	I	Y	L	L	16
38	47		I	I	Y	I	V	R	T	E	H	15
39	109		L	S	G	M	E	S	T	V	L	15
40	114		S	T	V	L	L	A	M	A	F	15
41	123		D	R	Y	V	A	I	C	H	P	15
42	145		K	I	G	V	A	A	V	V	R	15
43	156		A	L	M	A	P	L	P	V	F	15
44	168		L	P	F	C	R	S	N	I	L	15
45	172		R	S	N	I	L	S	H	S	Y	15
46	198		V	V	Y	G	L	I	V	I	I	15
47	206		I	S	A	I	G	L	D	S	L	15
48	229		G	L	T	R	E	A	Q	A	K	15
49	248		A	V	F	I	F	Y	V	P	F	15

HLA-B*2705 nonomers(SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
50	251	I F Y V P F I G L	15
51	274	P V I L A N I Y L	15
52	290	P I V Y G V K T K	15
53	298	K E I R Q R I L R	15
54	19	L P G L E E A Q F	14
55	29	L A F P L C S L Y	14
56	30	A F P L C S L Y L	14
57	39	I A V L G N L T I	14
58	40	A V L G N L T I I	14
59	79	S M P K M L A I F	14
60	81	P K M L A I F W F	14
61	99	C L L Q I F A I H	14
62	137	V L T L P R V T K	14
63	138	L T L P R V T K I	14
64	150	A V V R G A A L M	14
65	160	P L P V F I K Q L	14
66	174	N I L S H S Y C L	14
67	180	Y C L H Q D V M K	14
68	192	D D I R V N V V Y	14
69	212	D S L L I S F S Y	14
70	213	S L L I S F S Y L	14
71	214	L L I S F S Y L L	14
72	260	S M V H R F S K R	14
73	263	H R F S K R R D S	14
74	267	K R R D S P L P V	14
75	293	Y G V K T K E I R	14
76	301	R Q R I L R L F H	14
77	302	Q R I L R L F H V	14
78	5	N G N E S S A T Y	13
79	23	E E A Q F W L A F	13
80	28	W L A F P L C S L	13
81	44	N L T I I Y I V R	13
82	51	V R T E H S L H E	13
83	56	S L H E P M Y I F	13
84	60	P M Y I F L C M L	13
85	72	D I L I S T S S M	13
86	74	L I S T S S M P K	13
87	75	I S T S S M P K M	13
88	98	A C L L Q I F A I	13
89	104	F A I H S L S G M	13
90	110	S G M E S T V L L	13
91	116	V L L A M A F D R	13
92	126	V A I C H P L R H	13
93	149	A A V V R G A A L	13
94	158	M A P L P V F I K	13
95	164	F I K Q L P F C R	13
96	170	F C R S N I L S H	13
97	171	C R S N I L S H S	13
98	187	M K L A C D D I R	13

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
99	217	S	F	S	Y	L	L	I	L	K	13
100	224	L	K	T	V	L	G	L	T	R	13
101	242	C	V	S	H	V	C	A	V	F	13
102	256	F	I	G	L	S	M	V	H	R	13
103	261	M	V	H	R	F	S	K	R	R	13
104	49	Y	I	V	R	T	E	H	S	L	12
105	57	L	H	E	P	M	Y	I	F	L	12
106	88	W	F	N	S	T	T	I	Q	F	12
107	96	F	D	A	C	L	L	Q	I	F	12
108	134	H	A	T	V	L	T	L	P	R	12
109	152	V	R	G	A	A	L	M	A	P	12
110	179	S	Y	C	L	H	Q	D	V	M	12
111	197	N	V	V	Y	G	L	I	V	I	12
112	244	S	H	V	C	A	V	F	I	F	12
113	265	F	S	K	R	R	D	S	P	L	12
114	273	L	P	V	I	L	A	N	I	Y	12
115	285	P	P	V	L	N	P	I	V	Y	12
116	288	L	N	P	I	V	Y	G	V	K	12
117	296	K	T	K	E	I	R	Q	R	I	12
118	297	T	K	E	I	R	Q	R	I	L	12

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	24
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	H	A	T	V	L	T	L	22
4	267	K	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	I	L	R	L	F	20
6	231	T	R	E	A	Q	A	K	A	F	19
7	302	Q	R	I	L	R	L	F	H	V	19
8	124	R	Y	V	A	I	C	H	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	I	V	15
11	216	I	S	F	S	Y	L	L	I	L	15
12	11	A	T	Y	F	I	L	I	G	L	14
13	25	A	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	M	A	P	L	14
15	174	N	I	L	S	H	S	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	H	R	F	14
18	280	I	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	A	T	Y	F	13
20	14	F	I	L	I	G	L	P	G	L	13
21	21	G	L	E	E	A	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
23	130	H P L R H A T V L	13
24	201	G L I V I I S A I	13
25	203	I V I I S A I G L	13
26	214	L L I S F S Y L L	13
27	251	I F Y V P F I G L	13
28	263	H R F S K R R D S	13
29	275	V I L A N I Y L L	13
30	305	L R L F H V A T H	13
31	30	A F P L C S L Y L	12
32	34	C S L Y L I A V L	12
33	37	Y L I A V L G N L	12
34	51	V R T E H S L H E	12
35	60	P M Y I F L C M L	12
36	75	I S T S S M P K M	12
37	93	T I Q F D A C L L	12
38	123	D R Y V A I C H P	12
39	135	A T V L T L P R V	12
40	138	L T L P R V T K I	12
41	149	A A V V R G A A L	12
42	155	A A L M A P L P V	12
43	168	L P F C R S N I L	12
44	181	C L H Q D V M K L	12
45	188	K L A C D D I R V	12
46	190	A C D D I R V N V	12
47	195	R V N V V Y G L I	12
48	210	G L D S L L I S F	12
49	213	S L L I S F S Y L	12
50	220	Y L L I L K T V L	12
51	248	A V F I F Y V P F	12
52	279	N I Y L L V P P V	12
53	287	V L N P I V Y G V	12
54	296	K T K E I R Q R I	12
55	299	E I R Q R I L R L	12

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	39	I A V L G N L T I	26
2	31	F P L C S L Y L I	25
3	120	M A F D R Y V A I	24
4	130	H P L R H A T V L	23
5	118	L A M A F D R Y V	22
6	140	L P R V T K I G V	22
7	155	A A L M A P L P V	22
8	42	L G N L T I I Y I	21
9	254	V P F I G L S M V	21
10	284	V P P V L N P I V	21

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
11	168	L P F C R S N I L	20
12	235	Q A K A F G T C V	20
13	138	L T L P R V T K I	19
14	159	A P L P V F I K Q	18
15	189	L A C D D I R V N	18
16	198	V V Y G L I V I I	18
17	277	L A N I Y L L V P	18
18	207	S A I G L D S L L	17
19	283	L V P P V L N P I	17
20	63	I F L C M L S G I	16
21	86	I F W F N S T T I	16
22	110	S G M E S T V L L	16
23	144	T K I G V A A V V	16
24	149	A A V V R G A A L	16
25	197	N V V Y G L I V I	16
26	271	S P L P V I L A N	16
27	280	I Y L L V P P V L	16
28	3	D P N G N E S S A	15
29	40	A V L G N L T I I	15
30	97	D A C L L Q I F A	15
31	132	L R H A T V L T L	15
32	222	L I L K T V L G L	15
33	279	N I Y L L V P P V	15
34	285	P P V L N P I V Y	15
35	289	N P I V Y G V K T	15
36	9	S S A T Y F I L I	14
37	65	L C M L S G I D I	14
38	84	L A I F W F N S T	14
39	126	V A I C H P L R H	14
40	157	L M A P L P V F I	14
41	158	M A P L P V F I K	14
42	191	C D D I R V N V V	14
43	200	Y G L I V I I S A	14
44	209	I G L D S L L I S	14
45	215	L I S F S Y L L I	14
46	219	S Y L L I L K T V	14
47	220	Y L L I L K T V L	14
48	237	K A F G T C V S H	14
49	247	C A V F I F Y V P	14
50	249	V F I F Y V P F I	14
51	251	I F Y V P F I G L	14
52	257	I G L S M V H R F	14
53	268	R R D S P L P V I	14
54	273	L P V I L A N I Y	14
55	29	L A F P L C S L Y	13
56	33	L C S L Y L I A V	13
57	55	H S L H E P M Y I	13
58	67	M L S G I D I L I	13
59	80	M P K M L A I F W	13

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
60	95	Q	F	D	A	C	L	L	Q	I	13
61	98	A	C	L	L	Q	I	F	A	I	13
62	104	F	A	I	H	S	L	S	G	M	13
63	146	I	G	V	A	A	V	V	R	G	13
64	148	V	A	A	V	V	R	G	A	A	13
65	153	R	G	A	A	L	M	A	P	L	13
66	233	E	A	Q	A	K	A	F	G	T	13
67	243	V	S	H	V	C	A	V	F	I	13
68	292	V	Y	G	V	K	T	K	E	I	13
69	296	K	T	K	E	I	R	Q	R	I	13

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Please replace Table XXVII, beginning at page 201, line 1, with the following rewritten
Table XXVII:

--Table XXVII:

HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS
2133-2153, respectively in
order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	D	I	R	V	N	V	V	Y	27
2	244	S	H	V	C	A	V	F	I	F	Y	24
3	40	A	V	L	G	N	L	T	I	I	Y	21
4	284	V	P	P	V	L	N	P	I	V	Y	21
5	116	V	L	L	A	M	A	F	D	R	Y	20
6	28	W	L	A	F	P	L	C	S	L	Y	18
7	297	T	K	E	I	R	Q	R	I	L	R	17
8	21	G	L	E	E	A	Q	F	W	L	A	16
9	22	L	E	E	A	Q	F	W	L	A	F	16
10	52	R	T	E	H	S	L	H	E	P	M	16
11	53	T	E	H	S	L	H	E	P	M	Y	16
12	57	L	H	E	P	M	Y	I	F	L	C	16
13	111	G	M	E	S	T	V	L	L	A	M	16
14	272	P	L	P	V	I	L	A	N	I	Y	16
15	1	M	V	D	P	N	G	N	E	S	S	15
16	4	P	N	G	N	E	S	S	A	T	Y	15
17	121	A	F	D	R	Y	V	A	I	C	H	15
18	171	C	R	S	N	I	L	S	H	S	Y	15
19	211	L	D	S	L	L	I	S	F	S	Y	15
20	8	E	S	S	A	T	Y	F	I	L	I	13
21	190	A	C	D	D	I	R	V	N	V	V	13

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	score
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HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
1 221	L	L	I	L	K	<u>T</u>	V	L	G	L	30
2 100	L	L	Q	I	F	<u>A</u>	I	H	S	L	29
3 282	L	L	V	P	P	<u>V</u>	L	N	P	I	27
4 205	I	I	S	A	I	<u>G</u>	L	D	S	L	26
5 213	S	L	L	I	S	<u>F</u>	S	Y	L	L	25
6 56	S	L	H	E	P	<u>M</u>	Y	I	F	L	24
7 62	Y	I	F	L	C	<u>M</u>	L	S	G	I	24
8 108	S	L	S	G	M	<u>E</u>	S	T	V	L	24
9 117	L	L	A	M	A	<u>F</u>	D	R	Y	V	24
10 131	P	L	R	H	A	<u>T</u>	V	L	T	L	24
11 137	V	L	T	L	P	<u>R</u>	V	T	K	I	24
12 215	L	I	S	F	S	<u>Y</u>	L	L	I	L	24
13 38	L	I	A	V	L	<u>G</u>	N	L	T	I	23
14 41	V	L	G	N	L	<u>T</u>	I	I	Y	I	23
15 156	A	L	M	A	P	<u>L</u>	P	V	F	I	23
16 193	D	I	R	V	N	<u>V</u>	V	Y	G	L	23
17 214	L	L	I	S	F	<u>S</u>	Y	L	L	I	23
18 32	P	L	C	S	L	<u>Y</u>	L	I	A	V	22
19 119	A	M	A	F	D	<u>R</u>	Y	V	A	I	22
20 237	K	A	F	G	T	<u>C</u>	V	S	H	V	22
21 275	V	I	L	A	N	<u>I</u>	Y	L	L	V	22
22 85	A	I	F	W	F	<u>N</u>	S	T	T	I	21
23 139	T	L	P	R	V	<u>T</u>	K	I	G	V	21
24 202	L	I	V	I	I	<u>S</u>	A	I	G	L	21
25 13	Y	F	I	L	I	<u>G</u>	L	P	G	L	20
26 16	L	I	G	L	P	<u>G</u>	L	E	E	A	20
27 29	L	A	F	P	L	<u>C</u>	S	L	Y	L	20
28 142	R	V	T	K	I	<u>G</u>	V	A	A	V	20
29 148	V	A	A	V	V	<u>R</u>	G	A	A	L	20
30 167	Q	L	P	F	C	<u>R</u>	S	N	I	L	20
31 180	Y	C	L	H	Q	<u>D</u>	V	M	K	L	20
32 222	L	I	L	K	T	<u>V</u>	L	G	L	T	20
33 240	G	T	C	V	S	<u>H</u>	V	C	A	V	20
34 248	A	V	F	I	F	<u>Y</u>	V	P	F	I	20
35 250	F	I	F	Y	V	<u>P</u>	F	I	G	L	20
36 271	S	P	L	P	V	<u>I</u>	L	A	N	I	20
37 279	N	I	Y	L	L	<u>V</u>	P	P	V	L	20
38 304	I	L	R	L	F	<u>H</u>	V	A	T	H	20
39 10	S	A	T	Y	F	<u>I</u>	L	I	G	L	19
40 15	I	L	I	G	L	<u>P</u>	G	L	E	E	19
41 27	F	W	L	A	F	<u>P</u>	L	C	S	L	19
42 35	S	L	Y	L	I	<u>A</u>	V	L	G	N	19
43 37	Y	L	I	A	V	<u>L</u>	G	N	L	T	19
44 44	N	L	T	I	I	<u>Y</u>	I	V	R	T	19
45 64	F	L	C	M	L	<u>S</u>	G	I	D	I	19
46 83	M	L	A	I	F	<u>W</u>	F	N	S	T	19
47 159	A	P	L	P	V	<u>F</u>	I	K	Q	L	19
48 189	L	A	C	D	D	<u>I</u>	R	V	N	V	19
49 207	S	A	I	G	L	<u>D</u>	S	L	L	I	19
50 253	Y	V	P	F	I	<u>G</u>	L	S	M	V	19

HLA-A*0201 decamers (SEQ ID NOS 2154-2253, respectively in order of appearance)												
	Pos	1	2	3	4	5	6	7	8	9	0	score
51	276	I	L	A	N	I	<u>Y</u>	L	L	V	P	19
52	281	Y	L	L	V	P	<u>P</u>	V	L	N	P	19
53	283	L	V	P	P	V	<u>L</u>	N	P	I	V	19
54	286	P	V	L	N	P	<u>I</u>	V	Y	G	V	19
55	33	L	C	S	L	Y	<u>L</u>	I	A	V	L	18
56	36	L	Y	L	I	A	<u>V</u>	L	G	N	L	18
57	39	I	A	V	L	G	<u>N</u>	L	T	I	I	18
58	42	L	G	N	L	T	<u>I</u>	I	Y	I	V	18
59	66	C	M	L	S	G	<u>I</u>	D	I	L	I	18
60	111	G	M	E	S	T	<u>V</u>	L	L	A	M	18
61	128	I	C	H	P	L	<u>R</u>	H	A	T	V	18
62	134	H	A	T	V	L	<u>T</u>	L	P	R	V	18
63	154	G	A	A	L	M	<u>A</u>	P	L	P	V	18
64	157	L	M	A	P	L	<u>P</u>	V	F	I	K	18
65	190	A	C	D	D	I	<u>R</u>	V	N	V	V	18
66	229	G	L	T	R	E	<u>A</u>	Q	A	K	A	18
67	245	H	V	C	A	V	<u>F</u>	I	F	Y	V	18
68	274	P	V	I	L	A	<u>N</u>	I	Y	L	L	18
69	278	A	N	I	Y	L	<u>L</u>	V	P	P	V	18
70	291	I	V	Y	G	V	<u>K</u>	T	K	E	I	18
71	298	K	<u>E</u>	I	R	Q	<u>R</u>	I	L	R	L	18
72	48	I	Y	I	V	R	<u>T</u>	E	H	S	L	17
73	65	L	C	M	L	S	<u>G</u>	I	D	I	L	17
74	67	M	L	S	G	I	<u>D</u>	I	L	I	S	17
75	74	L	I	S	T	S	<u>S</u>	M	P	K	M	17
76	91	S	T	T	I	Q	<u>F</u>	D	A	C	L	17
77	94	I	Q	F	D	A	<u>C</u>	L	L	Q	I	17
78	188	K	L	A	C	D	<u>D</u>	I	R	V	N	17
79	197	N	V	V	Y	G	<u>L</u>	I	V	I	I	17
80	200	Y	G	L	I	V	<u>I</u>	I	S	A	I	17
81	218	F	<u>S</u>	Y	L	L	<u>I</u>	L	K	T	V	17
82	227	V	L	G	L	T	<u>R</u>	E	A	Q	A	17
83	303	R	I	L	R	L	<u>F</u>	H	V	A	T	17
84	21	G	L	E	E	A	<u>Q</u>	F	W	L	A	16
85	92	T	T	I	Q	F	<u>D</u>	A	C	L	L	16
86	97	D	A	C	L	L	<u>Q</u>	I	F	A	I	16
87	127	A	I	C	H	P	<u>L</u>	R	H	A	T	16
88	143	V	T	K	I	G	<u>V</u>	A	A	V	V	16
89	195	R	V	N	V	V	<u>Y</u>	G	L	I	V	16
90	220	Y	L	L	I	L	<u>K</u>	T	V	L	G	16
91	296	K	T	K	E	I	<u>R</u>	Q	R	I	L	16
92	18	G	L	P	G	L	<u>E</u>	E	A	Q	F	15
93	30	A	<u>F</u>	P	L	C	<u>S</u>	L	Y	L	I	15
94	126	V	A	I	C	H	<u>P</u>	L	R	H	A	15
95	145	K	I	G	V	A	<u>A</u>	V	V	R	G	15
96	173	S	N	I	L	S	<u>H</u>	S	Y	C	L	15
97	201	G	L	I	V	I	<u>I</u>	S	A	I	G	15
98	208	A	I	G	L	D	<u>S</u>	L	L	I	S	15
99	210	G	L	D	S	L	<u>L</u>	I	S	F	S	15
100	267	K	R	R	D	S	<u>P</u>	L	P	V	I	15

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	<u>R</u>	V	T	K	I	<u>G</u>	V	A	A	19
2	147	G	<u>V</u>	A	A	V	V	<u>R</u>	G	A	A	19
3	112	M	<u>E</u>	S	T	V	L	<u>L</u>	A	M	A	18
4	227	V	<u>L</u>	G	L	T	R	<u>E</u>	A	Q	A	18
5	229	G	<u>L</u>	T	R	E	A	<u>Q</u>	A	K	A	18
6	142	R	<u>V</u>	T	K	I	G	<u>V</u>	A	A	V	17
7	148	V	<u>A</u>	A	V	V	R	<u>G</u>	A	A	L	17
8	2	V	<u>D</u>	P	N	G	N	<u>E</u>	S	S	A	10
9	16	L	<u>I</u>	G	L	P	G	<u>L</u>	E	E	A	10
10	21	G	<u>L</u>	E	E	A	Q	<u>F</u>	W	L	A	10
11	31	F	<u>P</u>	L	C	S	L	<u>Y</u>	L	I	A	10
12	76	S	<u>T</u>	S	S	M	P	K	M	L	A	10
13	89	F	<u>N</u>	S	T	T	I	<u>Q</u>	F	D	A	10
14	96	F	<u>D</u>	A	C	L	L	<u>Q</u>	I	F	A	10
15	110	S	<u>G</u>	M	E	S	T	V	L	L	A	10
16	118	L	<u>A</u>	M	A	F	D	R	Y	V	A	10
17	126	V	<u>A</u>	I	C	H	P	<u>L</u>	R	H	A	10
18	140	L	<u>P</u>	R	V	T	K	<u>I</u>	G	V	A	10
19	146	I	<u>G</u>	V	A	A	V	V	R	G	A	10
20	150	A	<u>V</u>	V	R	G	A	<u>A</u>	L	M	A	10
21	181	C	<u>L</u>	H	Q	D	V	<u>M</u>	K	L	A	10
22	199	V	<u>Y</u>	G	L	I	V	<u>I</u>	I	S	A	10
23	225	K	<u>T</u>	V	L	G	L	T	R	E	A	10
24	239	F	<u>G</u>	T	C	V	S	<u>H</u>	V	C	A	10
25	269	R	<u>D</u>	S	P	L	P	<u>V</u>	I	L	A	10
26	302	Q	<u>R</u>	I	L	R	L	<u>F</u>	H	V	A	10
27	305	L	<u>R</u>	L	F	H	V	<u>A</u>	T	H	A	10
28	3	D	<u>P</u>	N	G	N	E	<u>S</u>	S	A	T	9
29	17	I	<u>G</u>	L	P	G	L	E	E	A	Q	9
30	22	L	<u>E</u>	E	A	Q	<u>F</u>	W	L	A	F	9
31	32	P	<u>L</u>	C	S	L	<u>Y</u>	L	I	A	V	9
32	77	T	<u>S</u>	S	M	P	K	<u>M</u>	L	A	I	9
33	90	N	<u>S</u>	T	T	I	Q	<u>F</u>	D	A	C	9
34	97	D	<u>A</u>	C	L	L	<u>Q</u>	I	F	A	I	9
35	111	G	<u>M</u>	E	S	T	V	<u>L</u>	L	A	M	9
36	113	E	<u>S</u>	T	V	L	L	<u>A</u>	M	A	F	9
37	119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	I	9
38	127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	T	9
39	151	V	<u>V</u>	R	G	A	A	<u>L</u>	M	A	P	9
40	182	L	<u>H</u>	Q	D	V	<u>M</u>	K	L	A	C	9
41	200	Y	<u>G</u>	L	I	V	<u>I</u>	I	S	A	I	9
42	226	T	<u>V</u>	L	G	L	T	<u>R</u>	E	A	Q	9
43	228	L	<u>G</u>	L	T	R	E	<u>A</u>	Q	A	K	9

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
44 230	L	<u>T</u>	R	E	A	Q	<u>A</u>	K	A	F	9
45 240	G	<u>T</u>	C	V	S	H	<u>V</u>	C	A	V	9
46 270	D	<u>S</u>	P	L	P	V	<u>I</u>	L	A	N	9
47 303	R	<u>I</u>	L	R	L	F	<u>H</u>	V	A	T	9
48 306	R	<u>L</u>	F	H	V	A	<u>T</u>	H	A	S	9

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
1 299	E	I	R	Q	R	I	L	R	L	F	31
2 193	D	I	R	V	N	V	V	Y	G	L	29
3 250	F	I	F	Y	V	P	F	I	G	L	25
4 256	F	I	G	L	S	M	V	H	R	F	25
5 74	L	I	S	T	S	S	M	P	K	M	24
6 274	P	V	I	L	A	N	I	Y	L	L	24
7 18	G	L	P	G	L	E	E	A	Q	F	23
8 116	V	L	L	A	M	A	F	D	R	Y	23
9 205	I	I	S	A	I	G	L	D	S	L	23
10 221	L	L	I	L	K	T	V	L	G	L	23
11 230	L	T	R	E	A	Q	A	K	A	F	23
12 13	Y	F	I	L	I	G	L	P	G	L	22
13 40	A	V	L	G	N	L	T	I	I	Y	22
14 56	S	L	H	E	P	M	Y	I	F	L	22
15 95	Q	F	D	A	C	L	L	Q	I	F	22
16 215	L	I	S	F	S	Y	L	L	I	L	22
17 92	T	T	I	Q	F	D	A	C	L	L	21
18 100	L	L	Q	I	F	A	I	H	S	L	21
19 103	I	F	A	I	H	S	L	S	G	M	21
20 296	K	T	K	E	I	R	Q	R	I	L	21
21 28	W	L	A	F	P	L	C	S	L	Y	20
22 131	P	L	R	H	A	T	V	L	T	L	20
23 59	E	P	M	Y	I	F	L	C	M	L	19
24 91	S	T	T	I	Q	F	D	A	C	L	19
25 202	L	I	V	I	I	S	A	I	G	L	19
26 212	D	S	L	L	I	S	F	S	Y	L	19
27 272	P	L	P	V	I	L	A	N	I	Y	19
28 279	N	I	Y	L	L	V	P	P	V	L	19
29 52	R	T	E	H	S	L	H	E	P	M	18
30 62	Y	I	F	L	C	M	L	S	G	I	18
31 72	D	I	L	I	S	T	S	S	M	P	18
32 108	S	L	S	G	M	E	S	T	V	L	18
33 113	E	S	T	V	L	L	A	M	A	F	18
34 151	V	V	R	G	A	A	L	M	A	P	18
35 78	S	S	M	P	K	M	L	A	I	F	17
36 142	R	V	T	K	I	G	V	A	A	V	17
37 162	P	V	F	I	K	Q	L	P	F	C	17
38 164	F	I	K	Q	L	P	F	C	R	S	17

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
39	167	Q	L	P	F	C	R	S	N	I	L	17
40	185	D	V	M	K	L	A	C	D	D	I	17
41	248	A	V	F	I	F	Y	V	P	F	I	17
42	253	Y	V	P	F	I	G	L	S	M	V	17
43	45	L	T	I	I	Y	I	V	R	T	E	16
44	145	K	I	G	V	A	A	V	V	R	G	16
45	198	V	V	Y	G	L	I	V	I	I	S	16
46	203	I	V	I	I	S	A	I	G	L	D	16
47	209	I	G	L	D	S	L	L	I	S	F	16
48	213	S	L	L	I	S	F	S	Y	L	L	16
49	255	P	F	I	G	L	S	M	V	H	R	16
50	264	R	F	S	K	R	R	D	S	P	L	16
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	V	<u>L</u>	T	L	<u>P</u>	<u>R</u>	V	T	K	31
2	287	V	L	<u>N</u>	P	I	<u>V</u>	<u>Y</u>	G	V	K	28
3	223	I	<u>L</u>	<u>K</u>	T	V	<u>L</u>	<u>G</u>	L	T	R	27
4	304	I	<u>L</u>	<u>R</u>	L	F	<u>H</u>	<u>V</u>	A	T	H	27
5	73	I	L	<u>I</u>	S	T	<u>S</u>	<u>S</u>	M	P	K	26
6	15	I	<u>L</u>	<u>I</u>	G	L	<u>P</u>	<u>G</u>	L	E	E	23
7	40	A	V	<u>L</u>	G	N	<u>L</u>	T	I	I	Y	23
8	150	A	V	<u>V</u>	R	G	<u>A</u>	<u>A</u>	L	M	A	23
9	258	G	L	<u>S</u>	M	V	<u>H</u>	<u>R</u>	F	S	K	23
10	18	G	L	<u>P</u>	G	L	<u>E</u>	<u>E</u>	A	Q	F	22
11	303	R	I	<u>L</u>	R	L	<u>F</u>	<u>H</u>	V	A	T	22
12	276	I	L	<u>A</u>	N	I	<u>Y</u>	<u>L</u>	L	V	P	21
13	28	W	L	<u>A</u>	F	P	<u>L</u>	<u>C</u>	S	L	Y	20
14	115	T	V	<u>L</u>	L	A	<u>M</u>	<u>A</u>	F	D	R	20
15	116	V	L	<u>L</u>	A	M	<u>A</u>	<u>F</u>	D	R	Y	20
16	125	Y	V	<u>A</u>	I	C	<u>H</u>	P	L	R	H	20
17	131	P	L	<u>R</u>	H	A	T	<u>V</u>	L	T	L	20
18	144	T	K	I	G	V	A	A	V	V	R	20

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
19 156	A	L	<u>M</u>	A	P	<u>L</u>	P	V	F	I	20
20 195	R	V	<u>N</u>	V	V	<u>Y</u>	G	L	I	V	20
21 35	S	L	<u>Y</u>	L	I	<u>A</u>	V	L	G	N	19
22 272	P	L	<u>P</u>	V	I	<u>L</u>	A	N	I	Y	19
23 37	Y	L	<u>I</u>	A	V	<u>L</u>	G	N	L	T	18
24 49	Y	I	<u>V</u>	R	T	<u>E</u>	H	S	L	H	18
25 50	I	V	<u>R</u>	T	E	<u>H</u>	S	L	H	E	18
26 108	S	L	<u>S</u>	G	M	<u>E</u>	S	T	V	L	18
27 142	R	V	<u>T</u>	K	I	<u>G</u>	V	A	A	V	18
28 188	K	L	<u>A</u>	C	D	<u>D</u>	I	R	V	N	18
29 279	N	I	<u>Y</u>	L	L	<u>V</u>	P	P	V	L	18
30 291	I	V	<u>Y</u>	G	V	<u>K</u>	T	K	E	I	18
31 294	G	V	<u>K</u>	T	K	<u>E</u>	I	R	Q	R	18
32 46	T	I	<u>I</u>	Y	I	<u>V</u>	R	T	E	H	17
33 102	Q	I	<u>F</u>	A	I	<u>H</u>	S	L	S	G	17
34 151	V	V	<u>R</u>	G	A	<u>A</u>	L	M	A	P	17
35 179	S	Y	<u>C</u>	L	H	<u>Q</u>	D	V	M	K	17
36 203	I	V	<u>I</u>	I	S	<u>A</u>	I	G	L	D	17
37 204	V	I	<u>I</u>	S	A	<u>I</u>	G	L	D	S	17
38 220	Y	L	<u>L</u>	I	L	<u>K</u>	T	V	L	G	17
39 221	L	L	<u>I</u>	L	K	<u>T</u>	V	L	G	L	17
40 227	V	L	<u>G</u>	L	T	<u>R</u>	E	A	Q	A	17
41 242	C	V	<u>S</u>	H	V	<u>C</u>	A	V	F	I	17
42 289	N	P	<u>I</u>	V	Y	<u>G</u>	V	K	T	K	17
43 38	L	I	<u>A</u>	V	L	<u>G</u>	N	L	T	I	16
44 85	A	I	<u>F</u>	W	F	<u>N</u>	S	T	T	I	16
45 147	G	V	<u>A</u>	A	V	<u>V</u>	R	G	A	A	16
46 198	V	V	<u>Y</u>	G	L	<u>I</u>	V	I	I	S	16
47 201	G	L	<u>I</u>	V	I	<u>I</u>	S	A	I	G	16
48 214	L	L	<u>I</u>	S	F	<u>S</u>	Y	L	L	I	16
49 226	T	V	<u>L</u>	G	L	<u>T</u>	R	E	A	Q	16
50 228	L	G	<u>L</u>	T	R	<u>E</u>	A	Q	A	K	16
51 229	G	L	<u>T</u>	R	E	<u>A</u>	Q	A	K	A	16
52 1	M	V	<u>D</u>	P	N	<u>G</u>	N	E	S	S	15
53 44	N	L	<u>T</u>	I	I	<u>Y</u>	I	V	R	T	15
54 47	I	I	<u>Y</u>	I	V	<u>R</u>	T	E	H	S	15
55 67	M	L	<u>S</u>	G	I	<u>D</u>	I	L	I	S	15
56 72	D	I	<u>L</u>	I	S	<u>T</u>	S	S	M	P	15
57 99	C	L	<u>L</u>	Q	I	<u>F</u>	A	I	H	S	15
58 105	A	I	<u>H</u>	S	L	<u>S</u>	G	M	E	S	15
59 145	K	I	<u>G</u>	V	A	<u>A</u>	V	V	R	G	15
60 175	I	L	<u>S</u>	H	S	<u>Y</u>	C	L	H	Q	15
61 191	C	D	<u>D</u>	I	R	<u>V</u>	N	V	V	Y	15
62 208	A	I	<u>G</u>	L	D	<u>S</u>	L	L	I	S	15
63 275	V	I	<u>L</u>	A	N	<u>I</u>	Y	L	L	V	15
64 281	Y	L	<u>L</u>	V	P	<u>P</u>	V	L	N	P	15
65 299	E	I	<u>R</u>	Q	R	<u>I</u>	L	R	L	F	15
66 306	R	L	<u>F</u>	H	V	<u>A</u>	T	H	A	S	15

HLA-B*0702 decamers (SEQ ID

NOS 2433-2492, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score	
1	159	A	P	L	P	V	F	I	K	Q	L	23
2	59	E	P	M	Y	I	F	L	C	M	L	22
3	273	L	P	V	I	L	A	N	I	Y	L	20
4	3	D	P	N	G	N	E	S	S	A	T	19
5	130	H	P	L	R	H	A	T	V	L	T	19
6	140	L	P	R	V	T	K	I	G	V	A	19
7	161	L	P	V	F	I	K	Q	L	P	F	19
8	31	F	P	L	C	S	L	Y	L	I	A	18
9	271	S	P	L	P	V	I	L	A	N	I	18
10	80	M	P	K	M	L	A	I	F	W	F	16
11	108	S	L	S	G	M	E	S	T	V	L	16
12	131	P	L	R	H	A	T	V	L	T	L	15
13	264	R	F	S	K	R	R	D	S	P	L	15
14	33	L	C	S	L	Y	L	I	A	V	L	14
15	109	L	S	G	M	E	S	T	V	L	L	14
16	152	V	R	G	A	A	L	M	A	P	L	14
17	205	I	I	S	A	I	G	L	D	S	L	14
18	215	L	I	S	F	S	Y	L	L	I	L	14
19	268	R	R	D	S	P	L	P	V	I	L	14
20	29	L	A	F	P	L	C	S	L	Y	L	13
21	148	V	A	A	V	V	R	G	A	A	L	13
22	156	A	L	M	A	P	L	P	V	F	I	13
23	193	D	I	R	V	N	V	Y	G	L		13
24	221	L	L	I	L	K	T	V	L	G	L	13
25	298	K	E	I	R	Q	R	I	L	R	L	13
26	7	N	E	S	S	A	T	Y	F	I	L	12
27	19	L	P	G	L	E	E	A	Q	F	W	12
28	24	E	A	Q	F	W	L	A	F	P	L	12
29	119	A	M	A	F	D	R	Y	V	A	I	12
30	129	C	H	P	L	R	H	A	T	V	L	12
31	206	I	S	A	I	G	L	D	S	L	L	12
32	219	S	Y	L	L	I	L	K	T	V	L	12
33	279	N	I	Y	L	L	V	P	P	V	L	12
34	285	P	P	V	L	N	P	I	V	Y	G	12
35	8	E	S	S	A	T	Y	F	I	L	I	11
36	13	Y	F	I	L	I	G	L	P	G	L	11
37	27	F	W	L	A	F	P	L	C	S	L	11
38	48	I	Y	I	V	R	T	E	H	S	L	11
39	56	S	L	H	E	P	M	Y	I	F	L	11
40	65	L	C	M	L	S	G	I	D	I	L	11
41	75	I	S	T	S	S	M	P	K	M	L	11
42	77	T	S	S	M	P	K	M	L	A	I	11
43	91	S	T	T	I	Q	F	D	A	C	L	11
44	123	D	R	Y	V	A	I	C	H	P	L	11
45	142	R	V	T	K	I	G	V	A	A	V	11
46	180	Y	C	L	H	Q	D	V	M	K	L	11
47	190	A	C	D	D	I	R	V	N	V	V	11
48	212	D	S	L	L	I	S	F	S	Y	L	11
49	234	A	Q	A	K	A	F	G	T	C	V	11
50	242	C	V	S	H	V	C	A	V	F	I	11
51	248	A	V	F	I	F	Y	V	P	F	I	11

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
52	250	F	I	F	Y	V	P	F	I	G	L	11
53	254	V	P	F	I	G	L	S	M	V	H	11
54	266	S	K	R	R	D	S	P	L	P	V	11
55	267	K	R	R	D	S	P	L	P	V	I	11
56	269	R	D	S	P	L	P	V	I	L	A	11
57	278	A	N	I	Y	L	L	V	P	P	V	11
58	284	V	P	P	V	L	N	P	I	V	Y	11
59	289	N	P	I	V	Y	G	V	K	T	K	11
60	296	K	T	K	E	I	R	Q	R	I	L	11

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Please replace Table XXVIII, beginning at page 205, line 1, with the following rewritten
Table XXVIII:

--Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	36
2 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	34
3 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	33
4 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	32
5 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	31
6 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	31
7 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	31
8 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	30
9 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	30
10 240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	30
11 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	29
12 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	29
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	28
14 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	27
15 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	26
16 183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	26
17 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	26
18 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	25
19 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	25
20 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	25
21 70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	25
22 111	G	M	E	S	T	V	L	L	A	M	A	F	D	R	Y	25
23 148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	25
24 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	25
25 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	25
26 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	25

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
27 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	25
28 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	24
29 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	24
30 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	24
31 77	T	S	S	M	P	K	M	L	A	I	F	W	F	N	S	24
32 85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	24
33 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	24
34 151	V	V	R	G	A	A	L	M	A	P	L	P	V	F	I	24
35 161	L	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	24
36 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	24
37 202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	24
38 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	24
39 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	24
40 251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	24
41 83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	23
42 101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	23
43 165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	23
44 203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	23
45 221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	23
46 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	23
47 27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	22
48 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	22
49 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	22
50 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	22
51 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	22
52 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	22
53 146	I	G	V	A	A	V	V	R	G	A	A	L	M	A	P	22
54 154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	22
55 205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	22
56 243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	22
57 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	22
58 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	22
59 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	22
60 34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	21
61 69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	21
62 152	V	R	G	A	A	L	M	A	P	L	P	V	F	I	K	21
63 299	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	H	21
64 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
65 135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	20
66 141	P	R	V	T	K	I	G	V	A	A	V	V	R	G	A	20
67 191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	20
68 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
69 262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	20
70 271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	20
71 28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	19
72 58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	19
73 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	19
74 60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	19
75 98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	19
76 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	19
77 219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	19

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
78 228	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	19
79 232	R	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	19
80 246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	19
81 297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	19
82 3	D	P	N	G	N	E	S	S	A	T	Y	F	I	L	I	18
83 14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	18
84 25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	18
85 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	18
86 46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	18
87 78	S	S	M	P	K	M	L	A	I	F	W	F	N	S	T	18
88 84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	18
89 89	F	N	S	T	T	I	Q	F	D	A	C	L	L	Q	I	18
90 93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
91 115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	18
92 119	A	M	A	F	D	R	Y	V	A	I	C	H	P	L	R	18
93 127	A	I	C	H	P	L	R	H	A	T	V	L	T	L	P	18
94 129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	18
95 147	G	V	A	A	V	V	R	G	A	A	L	M	A	P	L	18
96 149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	18
97 216	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	18
98 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	18
99 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
100 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	18
101 284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	18
102 286	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	I	18
103 303	R	I	L	R	L	F	H	V	A	T	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	26
2 206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	23
3 91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	22
4 117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	22
5 38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	21
6 179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	21
7 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	21
8 219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	21
9 272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	21
10 26	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	20
11 114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	20
12 129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
13 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
14 186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
15 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
16 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	20
17 297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	20
18 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	19
19 54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	19

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
20 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	19
21 165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	19
22 191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	19
23 203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	19
24 213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	19
25 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	19
26 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	19
27 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	19
28 254	V	P	F	I	G	L	S	M	V	H	R	F	S	K	R	19
29 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	19
30 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	18
31 93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
32 98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	18
33 125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	18
34 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	18
35 187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
36 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	18
37 225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	18
38 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	18
39 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	18
40 18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	17
41 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	17
42 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	17
43 159	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	17
45 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
46 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	16
47 262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	16
48 294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49 46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	15
50 51	V	R	T	E	H	S	L	H	E	P	M	Y	I	F	L	15
51 172	R	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	15
52 189	L	A	C	D	D	I	R	V	N	V	V	Y	G	L	I	15
53 212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	15
54 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	15
55 271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	15
56 279	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	15
57 12	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	14
58 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	14
59 64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
60 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
61 273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
62 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	14
63 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	13
64 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	13
65 71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	13
66 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	13
67 109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68 113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
69 135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	13
70 195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	13
71 202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	13
72 220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	13
73 221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	13
74 264	R	F	S	K	R	R	D	S	P	L	P	V	I	L	A	13
75 280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	13
76 302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	26
2 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	26
3 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	26
4 83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	26
5 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	26
6 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	26
7 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	26
8 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	26
9 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	26
10 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	26
11 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	26
12 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	26
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	22
14 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	22
15 25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	22
16 34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	22
17 84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	22
18 122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	22
19 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	22
20 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	22
21 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	22
22 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	22
23 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	22
24 19	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	L	20
25 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	20
26 33	L	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	20
27 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	20
28 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	20
29 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	20
30 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	20
31 48	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	Y	20
32 58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	20
33 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	20
34 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	20
35 71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	20

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
36	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	20
37	81	P	K	M	L	A	I	F	W	F	N	S	T	T	I	Q	20
38	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	20
39	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	20
40	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	20
41	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
42	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	20
43	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	20
44	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	20
45	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	20
46	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	20
47	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
48	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
49	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	20
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	Y	G	L	I	V	I	I	S	A	20
57	196	V	N	V	Y	G	L	I	V	I	I	S	A	I	G	L	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16
99	236	A	K	A	F	G	T	C	V	S	H	V	C	A	V	F	16
100	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	16
101	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	14
105	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	14
106	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	14
107	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	14
108	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	14
109	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
110	70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	14
111	72	D	I	L	I	S	T	S	S	M	P	K	M	L	A	I	14
112	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	14
113	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	14
114	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	14
115	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	14
116	148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	14
117	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	14
118	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	14
119	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	M	14
121	184	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	V	14
122	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	14
123	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	14
124	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	14
126	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	14
127	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	14
129	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	14
133	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	14

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
134 302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	28
2 122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	25
3 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	25
4 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	24
5 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	23
6 255	P	F	I	G	L	S	M	V	H	R	F	S	K	R	R	23
7 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	22
8 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	22
10 237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	22
11 74	L	I	S	T	S	S	M	P	K	M	L	A	I	F	W	21
12 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
13 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
14 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
15 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
16 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	20
17 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18 290	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	I	20
19 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	19
22 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	19
23 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	19
24 247	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	19
25 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	19
26 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	18
27 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	18
28 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	18
29 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	18
30 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	18
32 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
33 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	17
34 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	17
35 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
36 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	17
37 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	17
38 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	16
39 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	16
40 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	16
41 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
42 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	15

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
43	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	15
44	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	15
45	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	15
46	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	15
47	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	15
48	260	S	M	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49	261	M	V	H	R	F	S	K	R	R	D	S	P	L	P	V	15
50	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	15
51	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	15
52	114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	14
53	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	14
54	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	14
55	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
56	170	F	C	R	S	N	I	L	S	H	S	Y	C	L	H	Q	14
57	180	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	I	14
58	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	14
59	229	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	V	14
60	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
61	298	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	14

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Please replace Table XXIX, beginning at page 213, line 1, with the following rewritten

Table XXIX:

--Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

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1 TGC GCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTAAATA GAGGCAGGGT TTCACCATGT
61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GCGGGGGCTT ATTGTTTTTT AAAAAGATTT
181 CCAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
241 TGTGTCAAT TACTTTAGAT GTTTCTATCA GGAAAGTTTG AGAAATGGTA TTCAGGCCCTA
301 AACACAAACC TCTCTTGAAA TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCTGTTGA
601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTTCTACTT TTCCCTTTCT ACTTTCTAG
841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCAATTG CCTCATCATT CGTGTGGAGA GGCGACTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCTT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG CTGTCCTGCT GGCCATGGCT TTTGACCGCT

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1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTACACACA CTCCTTCTGT CTGCACCAAG
1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGACTCAA GGCTTTCAAC ACCTGCATCT
1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
1741 CACCTGTAGT CAACCCCTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
1921 TTGTGCTGTC TTCTTCCAGC AATTTAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
1981 AGTACTGAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACTA GTCCCTCTGC
2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT
2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
2221 CCTAAAGTGG TTACCCAGCC ATAATCAGG GTTAATGAAG GTATTGCGG AATATTGAACT
2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT TCTGATGCAA
2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGACA CATGGAATAC
2521 GTRACTGTTG TGTCTGTTG AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
2581 ACGTGTCTCT GATTGCGCAT TTGTATTCTT GTGGTATCTG TTAGTTGGTA TATGATATGT
2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
2701 GGTAAGAATG CTGCCTCTAC CTTTCTCTCC TATTTGTACT ATGTGAATGT GGTGCATGAA
2761 TGTGTGGAAT GTGTGGAATG TGTAATATTG GGATGCCTGT ATCTTTCAGC GTGTTTGGGT
2821 GTATGTCCAT TGTGCATAAT ATTTGAGATG TAAAACCAT TGTGCGGTA TATGTGTTAT
2881 TAGTTGTAAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG GTACTGATGC
2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTTAAGGCAA ACTTCTTTTG TGTGTTGGGT
3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTCTCTGGC CTGGGGTCAG
3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
3241 TTTCACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGT
3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCTCCCTA AACCTGCCC
3361 TCCTGCCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTT GGCTTATCTG
3421 CCAAACATGT ATAAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAAC AATTAGCCGG
3481 GTGTGATGGC GCGTGCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCCTTCTGTT
3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAAGCATT ACCTCATTAT
3781 TCACCTTGTC TCATGTCTCA CTGTCCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
3841 GAAGTAGAAG TCCCTTTGGT ATTTTTTAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTGAGGCTG CGTGCTCTGT
3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAACT
4081 CACAGTTGTG AACTGATCA GTAAAAATA AGGGGAGACC AACTAAAAAC CATGTTGTTT
4141 TATTTATAGA TGTAAGTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTTG CCCTTAAGGG AGAAACCAGA
4261 TGTCAATGGT CTTACGTGGC TGGTGTGGG GGTGGGGAGG GTTAAAGAAA CCACGTTCTC
4321 TGTCTCTAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCAGTGTCC
4381 CTGGGGACCT TGTTTATAAG TTATCCAGAC ACAGGGACCA GAGCCTGGGA GACAAAAAAA
4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTCCA CGCTTAGCAA

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sd-79244

14-00000 14600 146000

5.

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                NF-1      CP2      NF-1
Query: 4506 gccaggcacagtggtctcacgcctgtaatcccaacaccatgggaggctgagatgggtggat 4565
(SEQ ID NO: 2876)
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 153 gccaggctacagtggtctcacgcctgtaatcccagcactttgggaggccgaggtgggcagat 94
(SEQ ID NO: 2877)

Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620
| | ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 93 cgcaagggtcagggggttcgagaccagccaggccaacatggtgaaacctgcctcta 39--

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REMARKS

The Specification has been amended to correct erroneous sequence identification numbers and include sequence identification numbers which were omitted at the time of filing.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made.".

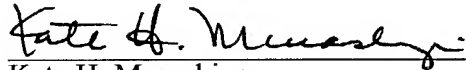
The undersigned hereby states that the compact disc copy of the Sequence Listing and the computer readable form copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the patent office determines that extensions and/or other relief is required, applicant petition for any required relief including extensions of time and authorize the assistant commissioner to charge the cost of such petitions and/or fees due to our deposit account no. 03-1952 under order no. 511582002420. The assistant commissioner is not authorized to charge the cost of the issue fee to the deposit account.

Respectfully submitted,

Dated: May 20, 2002

By:



Kate H. Murashige
Registration No. 29,959

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VERSION WITH MARKINGS TO SHOW CHANGES MADE**In the Specification:**

The paragraph beginning at page 7, line 21, has been amended as follows:

Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960). The 101P3A11 SSH sequence.

The paragraph beginning at page 7, line 22, has been amended as follows:

Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11. The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).

The paragraph beginning at page 7, line 26, has been amended as follows:

Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962). The 101P3A11 protein has 317 amino acids.

The paragraph beginning at page 7, line 28, has been amended as followsh:

Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963) The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25) predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.

The paragraph beginning at page 11, line 31, has been amended as follows:

Figure 23. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 1, has been amended as follows:

Figure 24. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 3, has been amended as follows:

Figure 25. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).

The paragraph beginning at page 36, line 20, has been amended as follows:

Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".

The paragraph beginning at page 37, line 25, has been amended as follows:

In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHis, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.

The paragraph beginning at page 70, line 3, has been amended as follows:

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; [SEQ ID NO: 710] (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; [SEQ ID NO: 711] (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; [SEQ ID NO: 712] (SEQ ID NO: 1405)). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

The paragraph beginning at page 70, line 11, has been amended as follows:

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa [SEQ ID NO: 713] (SEQ ID NO: 1406), where “X” is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all “L” natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

The paragraph beginning at page 80, line 16, has been amended as follows:

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant

polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

The paragraph beginning at page 86, line 29, has been amended as follows:

pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScissionTM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 8, has been amended as follows:

pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors

(New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 20, has been amended as follows:

pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.

The paragraph beginning at page 88, line 19, has been amended as follows:

pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 88, line 28, has been amended as follows:

pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 16, has been amended as follows:

PAPtag: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 27, has been amended as follows:

ptag5: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAptag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ-signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 90, line 30, has been amended as follows:

Additional pSRα constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.

The paragraph beginning at page 141, line 31, has been amended as follows:

The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; [SEQ ID NO:YY] (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in

293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.

Table XIX, beginning at page 186, has been amended as follows:

Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site

Number of matches: 3

- 1 7-10 NESS (SEQ ID NO: 1410)
- 2 44-47 NLTI (SEQ ID NO: 1411)
- 3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site

Number of matches: 3

- 1 56-59 SLHE (SEQ ID NO: 1414)
- 2 69-72 SGID (SEQ ID NO: 1415)
- 3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 1 6-11 GNESSA (SEQ ID NO: 1417)
- 2 21-26 GLEEAQ (SEQ ID NO: 1418)
- 3 111-116 GMESTV (SEQ ID NO: 1419)
- 4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature

112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)

Table XXI, beginning at page 190, line 1, has been amended as follows:

Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

```

1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNATAT
241 NATTCCTGCNG CTTGAGCATG ACACCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN

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361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCAA NNCNGGTACT
541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGNAA AAGGGGNAAN
661 CGGGGCGAAA TGNNAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA
781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG

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Table XXII, beginning at page 190, line 38, has been amended as follows:

Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89

Identities = 215/223 (96%), Gaps = 6/223 (2%)

Strand = Plus / Plus

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101P3A11: 68 cacattccttccatacgggttgagcctctacctgcctggtgctggtcacagttcagcttct 127
(SEQ ID NO: 1423)

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Variant : 1 cacattccttccatacgggttgagcctctacctgcctggtgctggtcacagttcagcttct 60
(SEQ ID NO: 1424)

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101P3A11: 128 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcacctaataaggcc 187
Variant : 61 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcacctaataaggcc 120

```

```

101P3A11: 188 tccctgggttagaagaggctcagttctggttgcccttccattgtgctccctctacctta 247
Variant : 121 tccctgggttagaagaggctcagttctggttgcc-tccattgtgctccctctanct-- 177

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101P3A11: 248 ttgctgtgctaggttaacttgacaatcatctacattgtgcggac 290
Variant : 178 atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcggac 217

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Table XXIII, beginning at page 191, line 8, has been amended as follows:

Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect (2) = 3e-29

Identities = 51/51 (100%)

Frame = +1 / +3

101P3A11: 70 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
(SEQ ID NO: 1425)

Variant : 3 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
(SEQ ID NO: 1426)

Table XXIV, beginning at page 191, line 16, has been amended as follows:

Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWGRXGVKMXPRVXECLCAKTSIMXTXYNGXESXXRKAKEXPXXGT LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPDRDGKRGXRGEMXKTGXRGXXKGXXXEG XGSREKXNXGXETXXXARXXKEXXXXXKSKSXGXKXGGXXXPXXXKNXXXGXSTRKXXG XXGK*XGNXXANRTXGKTPTGXAXRXXXPEXRX
Frame 2 (SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRGSLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAVHVPWQQDRAGTNGGEXG*RTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXXKXXXGAKXXKPGPGEXXRGXXVKD XVQGXKXTXGXKPPXXPGXERXXXXXKNXKKAXAXKXGEXXXXGRXKTXXGXXHGXXXA XKGNXXGTXKQTXRXERNPPEXXNAXXXPSXG
Frame 3 (SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTPIXLSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPRLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF NPAXGXXTGXXNKEGXXLGQNGXGXRTHGXXKGRXKGXGXGRNXKNRXPGXEGEXX*RT GFKGXKXPXRNXSXGPGXKGXGXGEXIXKKXXXKXGXXXTXXXXKXXXGXXXTEXXGR XREIXREXXKXKXGRNETHRXRXTXPPXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*) indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.

Table XXVI, beginning at page 193, line 1, has been amended as follows:

Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers										
	Pos	1	2	3	4	5	6	7	8	9 score
1	245	H	V	C	A	V	F	I	F	Y 24
2	29	L	A	F	P	L	C	S	L	Y 21
3	41	V	L	G	N	L	T	I	I	Y 21
4	285	P	P	V	L	N	P	I	V	Y 20
5	111	G	M	E	S	T	V	L	L	A 19
6	117	L	L	A	M	A	F	D	R	Y 19
7	172	R	S	N	I	L	S	H	S	Y 19
8	192	D	D	I	R	V	N	V	V	Y 19
9	212	D	S	L	L	I	S	F	S	Y 19
10	57	L	H	E	P	M	Y	I	F	L 18
11	22	L	E	E	A	Q	F	W	L	A 17
12	9	S	S	A	T	Y	F	I	L	I 16
13	52	R	T	E	H	S	L	H	E	P 16
14	54	E	H	S	L	H	E	P	M	Y 16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
15	78	S	S	M	P	K	M	L	A	I	16
16	95	Q	F	D	A	C	L	L	Q	I	16
17	159	A	P	L	P	V	F	I	K	Q	16
18	183	H	Q	D	V	M	K	L	A	C	16
19	1	M	V	D	P	N	G	N	E	S	15
20	5	N	G	N	E	S	S	A	T	Y	15
21	210	G	L	D	S	L	L	I	S	F	15
22	273	L	P	V	I	L	A	N	I	Y	15
23	271	S	P	L	P	V	I	L	A	N	14
24	91	S	T	T	I	Q	F	D	A	C	13
25	121	A	F	D	R	Y	V	A	I	C	13
26	138	L	T	L	P	R	V	T	K	I	13
27	218	F	S	Y	L	L	I	L	K	T	13
28	282	L	L	V	P	P	V	L	N	P	13
29	190	A	C	D	D	I	R	V	N	V	12
30	191	C	D	D	I	R	V	N	V	V	12
31	231	T	R	E	A	Q	A	K	A	F	12
32	268	R	R	D	S	P	L	P	V	I	12
33	270	D	S	P	L	P	V	I	L	A	12

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	L	N	P	I	V	Y	G	V	30
2	14	F	I	L	I	G	L	P	G	L	29
3	28	W	L	A	F	P	L	C	S	L	28
4	37	Y	L	I	A	V	L	G	N	L	28
5	222	L	I	L	K	T	V	L	G	L	28
6	66	C	M	L	S	G	I	D	I	L	26
7	108	S	L	S	G	M	E	S	T	V	26
8	181	C	L	H	Q	D	V	M	K	L	26
9	201	G	L	I	V	I	I	S	A	I	26
10	214	L	L	I	S	F	S	Y	L	L	26
11	275	V	I	L	A	N	I	Y	L	L	26
12	157	L	M	A	P	L	P	V	F	I	25
13	220	Y	L	L	I	L	K	T	V	L	25
14	276	I	L	A	N	I	Y	L	L	V	25
15	279	N	I	Y	L	L	V	P	P	V	25
16	138	L	T	L	P	R	V	T	K	I	24
17	213	S	L	L	I	S	F	S	Y	L	24
18	49	Y	I	V	R	T	E	H	S	L	23
19	143	V	T	K	I	G	V	A	A	V	23
20	188	K	L	A	C	D	D	I	R	V	23
21	198	V	V	Y	G	L	I	V	I	I	23
22	21	G	L	E	E	A	Q	F	W	L	22
23	40	A	V	L	G	N	L	T	I	I	22
24	206	I	S	A	I	G	L	D	S	L	22
25	11	A	T	Y	F	I	L	I	G	L	21
26	60	P	M	Y	I	F	L	C	M	L	21
27	135	A	T	V	L	T	L	P	R	V	21

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
28	160	P L P V F <u>I</u> K Q L	21
29	174	N I L S H <u>S</u> Y C L	21
30	207	S A I G L <u>D</u> S L L	21
31	272	P L P V I <u>L</u> A N I	21
32	283	L V P P V <u>L</u> N P I	21
33	67	M L S G I <u>D</u> I L I	20
34	101	L Q I F A <u>I</u> H S L	20
35	282	L L V P P <u>V</u> L N P	20
36	299	E I R Q R <u>I</u> L R L	20
37	304	I L R L F <u>H</u> V A T	20
38	39	I A V L G <u>N</u> L T I	19
39	45	L T I I Y <u>I</u> V R T	19
40	92	T T I Q F <u>D</u> A C L	19
41	110	S G M E S <u>T</u> V L L	19
42	127	A I C H P <u>L</u> R H A	19
43	132	L R H A T <u>V</u> L T L	19
44	149	A A V V R <u>G</u> A A L	19
45	155	A A L M A <u>P</u> L P V	19
46	156	A L M A P <u>L</u> P V F	19
47	203	I V I I S <u>A</u> I G L	19
48	208	A I G L D <u>S</u> L L I	19
49	216	I S F S Y <u>L</u> L I L	19
50	219	S Y L L I <u>L</u> K T V	19
51	221	L L I L K <u>T</u> V L G	19
52	223	I L K T V <u>L</u> G L T	19
53	17	I G L P G <u>L</u> E E A	18
54	33	L C S L Y <u>L</u> I A V	18
55	34	C S L Y L <u>I</u> A V L	18
56	38	L I A V L <u>G</u> N L T	18
57	43	G N L T I <u>I</u> Y I V	18
58	85	A I F W F <u>N</u> S T T	18
59	118	L A M A F <u>D</u> R Y V	18
60	194	I R V N V <u>V</u> Y G L	18
61	210	G L D S L <u>L</u> I S F	18
62	215	L I S F S <u>Y</u> L L I	18
63	246	V C A V F <u>I</u> F Y V	18
64	254	V P F I G <u>L</u> S M V	18
65	15	I L I G L <u>P</u> G L E	17
66	63	I F L C M <u>L</u> S G I	17
67	72	D I L I S <u>T</u> S S M	17
68	93	T I Q F D <u>A</u> C L L	17
69	98	A C L L Q <u>I</u> F A I	17
70	111	G M E S T <u>V</u> L L A	17
71	120	M A F D R <u>Y</u> V A I	17
72	167	Q L P F C <u>R</u> S N I	17
73	197	N V V Y G <u>L</u> I V I	17
74	226	T V L G L <u>T</u> R E A	17
75	281	Y L L V P <u>P</u> V L N	17
76	31	F P L C S <u>L</u> Y L I	16

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
77	56	S	L	H	E	P	<u>M</u>	Y	I	F	16
78	70	G	I	D	I	L	<u>I</u>	S	T	S	16
79	78	S	S	M	P	K	<u>M</u>	L	A	I	16
80	79	S	<u>M</u>	P	K	M	<u>L</u>	A	I	F	16
81	104	F	A	I	H	S	<u>L</u>	S	G	M	16
82	119	A	M	A	F	D	<u>R</u>	Y	V	A	16
83	144	T	K	I	G	V	<u>A</u>	A	V	V	16
84	147	G	V	A	A	V	<u>V</u>	R	G	A	16
85	186	V	M	K	L	A	<u>C</u>	D	D	I	16
86	230	L	T	R	E	A	<u>Q</u>	A	K	A	16
87	238	A	F	G	T	C	<u>V</u>	S	H	V	16
88	249	V	F	I	F	Y	<u>V</u>	P	F	I	16
89	302	Q	R	I	L	R	<u>L</u>	F	H	V	16
90	303	R	I	L	R	L	<u>F</u>	H	V	A	16
91	18	G	L	P	G	L	E	E	A	Q	15
92	35	S	L	Y	L	I	<u>A</u>	V	L	G	15
93	42	L	G	N	L	T	<u>I</u>	I	Y	I	15
94	46	T	I	I	Y	I	<u>V</u>	R	T	E	15
95	69	S	G	I	D	I	<u>L</u>	I	S	T	15
96	76	S	T	S	S	M	<u>P</u>	K	M	L	15
97	131	P	L	R	H	A	<u>T</u>	V	L	T	15
98	137	V	L	T	L	P	<u>R</u>	V	T	K	15
99	153	R	G	A	A	L	<u>M</u>	A	P	L	15
100	190	A	C	D	D	I	<u>R</u>	V	N	V	15
101	191	C	D	D	I	R	<u>V</u>	N	V	V	15
102	204	V	I	I	S	A	<u>I</u>	G	L	D	15
103	241	T	C	V	S	H	<u>V</u>	C	A	V	15
104	251	I	F	Y	V	P	<u>F</u>	I	G	L	15
105	269	R	D	S	P	L	<u>P</u>	V	I	L	15
106	280	I	Y	L	L	V	<u>P</u>	P	V	L	15
107	306	R	L	F	H	V	A	T	H	A	15

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
1	148	V	<u>A</u>	A	V	V	R	<u>G</u>	A	A	14
2	119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	13
3	147	G	<u>V</u>	A	A	V	V	<u>R</u>	G	A	12
4	97	D	<u>A</u>	C	L	L	Q	<u>I</u>	F	A	11
5	127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	10
6	3	D	<u>P</u>	N	G	N	E	<u>S</u>	S	A	9
7	17	I	<u>G</u>	L	P	G	L	<u>E</u>	E	A	9
8	22	L	<u>E</u>	E	A	Q	F	<u>W</u>	L	A	9
9	32	P	<u>L</u>	C	S	L	Y	<u>L</u>	I	A	9
10	77	T	<u>S</u>	S	M	P	K	<u>M</u>	L	A	9
11	90	N	<u>S</u>	T	T	I	Q	<u>F</u>	D	A	9
12	111	G	<u>M</u>	E	S	T	V	L	L	A	9

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
13	113	E	<u>S</u>	T	V	L	L	<u>A</u>	M	A	9
14	141	P	<u>R</u>	V	T	K	I	<u>G</u>	V	A	9
15	142	R	<u>V</u>	T	K	I	<u>G</u>	<u>V</u>	A	A	9
16	151	V	<u>V</u>	R	G	A	A	<u>L</u>	M	A	9
17	182	L	<u>H</u>	<u>Q</u>	D	V	M	<u>K</u>	L	A	9
18	200	Y	<u>G</u>	L	I	V	I	<u>I</u>	S	A	9
19	226	T	<u>V</u>	L	G	L	T	<u>R</u>	E	A	9
20	228	L	<u>G</u>	L	T	R	E	A	<u>Q</u>	A	9
21	230	L	<u>T</u>	R	E	A	<u>Q</u>	A	K	A	9
22	240	G	<u>T</u>	C	V	S	H	<u>V</u>	C	A	9
23	270	D	<u>S</u>	P	L	P	V	<u>I</u>	L	A	9
24	303	R	<u>I</u>	L	R	L	F	<u>H</u>	V	A	9
25	306	R	<u>L</u>	F	H	V	A	<u>T</u>	H	A	9

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19
30	150	A	V	V	R	G	A	A	L	M	19

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
31	174	N I L S H S Y C L	19
32	192	D D I R V N V V Y	19
33	214	L L I S F S Y L L	19
34	251	I F Y V P F I G L	19
35	8	E S S A T Y F I L	18
36	21	G L E E A Q F W L	18
37	45	L T I I Y I V R T	18
38	54	E H S L H E P M Y	18
39	59	E P M Y I F L C M	18
40	88	W F N S T T I Q F	18
41	93	T I Q F D A C L L	18
42	185	D V M K L A C D D	18
43	198	V V Y G L I V I I	18
44	62	Y I F L C M L S G	17
45	70	G I D I L I S T S	17
46	79	S M P K M L A I F	17
47	96	F D A C L L Q I F	17
48	104	F A I H S L S G M	17
49	138	L T L P R V T K I	17
50	143	V T K I G V A A V	17
51	204	V I I S A I G L D	17
52	212	D S L L I S F S Y	17
53	220	Y L L I L K T V L	17
54	256	F I G L S M V H R	17
55	283	L V P P V L N P I	17
56	29	L A F P L C S L Y	16
57	40	A V L G N L T I I	16
58	46	T I I Y I V R T E	16
59	52	R T E H S L H E P	16
60	75	I S T S S M P K M	16
61	91	S T T I Q F D A C	16
62	135	A T V L T L P R V	16
63	147	G V A A V V R G A	16
64	201	G L I V I I S A I	16
65	257	I G L S M V H R F	16
66	279	N I Y L L V P P V	16
67	30	A F P L C S L Y L	15
68	101	L Q I F A I H S L	15
69	115	T V L L A M A F D	15
70	127	A I C H P L R H A	15
71	153	R G A A L M A P L	15
72	163	V F I K Q L P F C	15
73	215	L I S F S Y L L I	15
74	216	I S F S Y L L I L	15
75	225	K T V L G L T R E	15
76	272	P L P V I L A N I	15
77	282	L L V P P V L N P	15
78	286	P V L N P I V Y G	15
79	287	V L N P I V Y G V	15

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	L	T	L	P	R	V	T	K	30
2	229	G	L	T	R	E	A	Q	A	K	27
3	145	K	I	G	V	A	A	V	V	R	26
4	150	A	V	V	R	G	A	A	L	M	24
5	290	P	I	V	Y	G	V	K	T	K	24
6	35	S	L	Y	L	I	A	V	L	G	23
7	156	A	L	M	A	P	L	P	V	F	23
8	47	I	I	Y	I	V	R	T	E	H	22
9	50	I	V	R	T	E	H	S	L	H	22
10	142	R	V	T	K	I	G	V	A	A	22
11	151	V	V	R	G	A	A	L	M	A	22
12	242	C	V	S	H	V	C	A	V	F	22
13	248	A	V	F	I	F	Y	V	P	F	22
14	116	V	L	L	A	M	A	F	D	R	21
15	192	D	D	I	R	V	N	V	V	Y	21
16	303	R	I	L	R	L	F	H	V	A	21
17	304	I	L	R	L	F	H	V	A	T	21
18	108	S	L	S	G	M	E	S	T	V	20
19	198	V	V	Y	G	L	I	V	I	I	20
20	291	I	V	Y	G	V	K	T	K	E	20
21	15	I	L	I	G	L	P	G	L	E	19
22	44	N	L	T	I	I	Y	I	V	R	19
23	73	I	L	I	S	T	S	S	M	P	19
24	74	L	I	S	T	S	S	M	P	K	19
25	99	C	L	L	Q	I	F	A	I	H	19
26	162	P	V	F	I	K	Q	L	P	F	19
27	203	I	V	I	I	S	A	I	G	L	19
28	221	L	L	I	L	K	T	V	L	G	19
29	245	H	V	C	A	V	F	I	F	Y	19
30	306	R	L	F	H	V	A	T	H	A	19
31	40	A	V	L	G	N	L	T	I	I	18
32	85	A	I	F	W	F	N	S	T	T	18
33	205	I	I	S	A	I	G	L	D	S	18
34	220	Y	L	L	I	L	K	T	V	L	18
35	253	Y	V	P	F	I	G	L	S	M	18
36	37	Y	L	I	A	V	L	G	N	L	17
37	41	V	L	G	N	L	T	I	I	Y	17
38	117	L	L	A	M	A	F	D	R	Y	17
39	131	P	L	R	H	A	T	V	L	T	17
40	136	T	V	L	T	L	P	R	V	T	17
41	180	Y	C	L	H	Q	D	V	M	K	17

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
42	201	G	L	I	V	I	I	S	A	I	17
43	213	S	L	L	I	S	F	S	Y	L	17
44	256	F	I	G	L	S	M	V	H	R	17
45	261	M	V	H	R	F	S	K	R	R	17
46	276	I	L	A	N	I	Y	L	L	V	17
47	281	Y	L	L	V	P	P	V	L	N	17
48	286	P	V	L	N	P	I	V	Y	G	17
49	288	L	N	P	I	V	Y	G	V	K	17
50	309	H	V	A	T	H	A	S	E	P	17
51	1	M	V	D	P	N	G	N	E	S	16
52	56	S	L	H	E	P	M	Y	I	F	16
53	70	G	I	D	I	L	I	S	T	S	16
54	72	D	I	L	I	S	T	S	S	M	16
55	115	T	V	L	L	A	M	A	F	D	16
56	125	Y	V	A	I	C	H	P	L	R	16
57	144	T	K	I	G	V	A	A	V	V	16
58	167	Q	L	P	F	C	R	S	N	I	16
59	175	I	L	S	H	S	Y	C	L	H	16
60	195	R	V	N	V	V	Y	G	L	I	16
61	197	N	V	V	Y	G	L	I	V	I	16
62	210	G	L	D	S	L	L	I	S	F	16
63	282	L	L	V	P	P	V	L	N	P	16
64	299	E	I	R	Q	R	I	L	R	L	16
65	301	R	Q	R	I	L	R	L	F	H	16
66	16	L	I	G	L	P	G	L	E	E	15
67	46	T	I	I	Y	I	V	R	T	E	15
68	102	Q	I	F	A	I	H	S	L	S	15
69	193	D	I	R	V	N	V	V	Y	G	15
70	208	A	I	G	L	D	S	L	L	I	15
71	223	I	L	K	T	V	L	G	L	T	15
72	237	K	A	F	G	T	C	V	S	H	15

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	P	L	R	H	A	T	V	L	22
2	59	E	P	M	Y	I	F	L	C	M	21
3	168	L	P	F	C	R	S	N	I	L	20
4	289	N	P	I	V	Y	G	V	K	T	19
5	3	D	P	N	G	N	E	S	S	A	18
6	19	L	P	G	L	E	E	A	Q	F	18
7	140	L	P	R	V	T	K	I	G	V	18
8	284	V	P	P	V	L	N	P	I	V	17
9	31	F	P	L	C	S	L	Y	L	I	16
10	254	V	P	F	I	G	L	S	M	V	16
11	269	R	D	S	P	L	P	V	I	L	16
12	149	A	A	V	V	R	G	A	A	L	15

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
13	153	R G A A L M A P L	15
14	156	A L M A P L P V F	15
15	251	I F Y V P F I G L	15
16	299	E I R Q R I L R L	15
17	8	E S S A T Y F I L	14
18	28	W L A F P L C S L	14
19	30	A F P L C S L Y L	14
20	110	S G M E S T V L L	14
21	132	L R H A T V L T L	14
22	159	A P L P V F I K Q	14
23	222	L I L K T V L G L	14
24	271	S P L P V I L A N	14
25	25	A Q F W L A F P L	13
26	109	L S G M E S T V L	13
27	124	R Y V A I C H P L	13
28	216	I S F S Y L L I L	13
29	268	R R D S P L P V I	13
30	280	I Y L L V P P V L	13
31	11	A T Y F I L I G L	12
32	34	C S L Y L I A V L	12
33	57	L H E P M Y I F L	12
34	76	S T S S M P K M L	12
35	142	R V T K I G V A A	12
36	151	V V R G A A L M A	12
37	190	A C D D I R V N V	12
38	194	I R V N V V Y G L	12
39	206	I S A I G L D S L	12
40	207	S A I G L D S L L	12
41	220	Y L L I L K T V L	12
42	267	K R R D S P L P V	12
43	304	I L R L F H V A T	12
44	14	F I L I G L P G L	11
45	23	E E A Q F W L A F	11
46	37	Y L I A V L G N L	11
47	40	A V L G N L T I I	11
48	77	T S S M P K M L A	11
49	78	S S M P K M L A I	11
50	80	M P K M L A I F W	11
51	92	T T I Q F D A C L	11
52	112	M E S T V L L A M	11
53	119	A M A F D R Y V A	11
54	127	A I C H P L R H A	11
55	131	P L R H A T V L T	11
56	155	A A L M A P L P V	11
57	157	L M A P L P V F I	11
58	181	C L H Q D V M K L	11
59	203	I V I I S A I G L	11
60	208	A I G L D S L L I	11
61	213	S L L I S F S Y L	11

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
62	248	A V F I F Y V P F	11
63	265	F S K R R D S P L	11
64	275	V I L A N I Y L L	11
65	285	P P V L N P I V Y	11

HLA-B*08 nonomers (SEQ ID
NOS 1813-1847, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	299	E I R Q R I L R L	31
2	265	F S K R R D S P L	29
3	149	A A V V R G A A L	24
4	168	L P F C R S N I L	24
5	294	G V K T K E I R Q	21
6	120	M A F D R Y V A I	20
7	292	V Y G V K T K E I	20
8	21	G L E E A Q F W L	19
9	78	S S M P K M L A I	19
10	160	P L P V F I K Q L	19
11	186	V M K L A C D D I	18
12	213	S L L I S F S Y L	18
13	221	L L I L K T V L G	18
14	296	K T K E I R Q R I	18
15	297	T K E I R Q R I L	18
16	130	H P L R H A T V L	17
17	181	C L H Q D V M K L	17
18	223	I L K T V L G L T	17
19	28	W L A F P L C S L	16
20	37	Y L I A V L G N L	16
21	56	S L H E P M Y I F	16
22	80	M P K M L A I F W	16
23	162	P V F I K Q L P F	16
24	201	G L I V I I S A I	16
25	207	S A I G L D S L L	16
26	214	L L I S F S Y L L	16
27	220	Y L L I L K T V L	16
28	233	E A Q A K A F G T	16
29	275	V I L A N I Y L L	16
30	304	I L R L F H V A T	16
31	14	F I L I G L P G L	15
32	110	S G M E S T V L L	15
33	138	L T L P R V T K I	15
34	164	F I K Q L P F C R	15
35	222	L I L K T V L G L	15

HLA-B*1510 nonomers (SEQ ID
NOS 1848-1890, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	score
1	57	L	H	E	P	M	Y	I	F	L	23
2	244	S	H	V	C	A	V	F	I	F	17
3	269	R	D	S	P	L	P	V	I	L	16
4	280	I	Y	L	L	V	P	P	V	L	16
5	262	V	H	R	F	S	K	R	R	D	15
6	299	E	I	R	Q	R	I	L	R	L	15
7	106	I	H	S	L	S	G	M	E	S	14
8	206	I	S	A	I	G	L	D	S	L	14
9	220	Y	L	L	I	L	K	T	V	L	14
10	251	I	F	Y	V	P	F	I	G	L	14
11	297	T	K	E	I	R	Q	R	I	L	14
12	21	G	L	E	E	A	Q	F	W	L	13
13	34	C	S	L	Y	L	I	A	V	L	13
14	54	E	H	S	L	H	E	P	M	Y	13
15	110	S	G	M	E	S	T	V	L	L	13
16	194	I	R	V	N	V	V	Y	G	L	13
17	8	E	S	S	A	T	Y	F	I	L	12
18	14	F	I	L	I	G	L	P	G	L	12
19	28	W	L	A	F	P	L	C	S	L	12
20	66	C	M	L	S	G	I	D	I	L	12
21	76	S	T	S	S	M	P	K	M	L	12
22	92	T	T	I	Q	F	D	A	C	L	12
23	109	L	S	G	M	E	S	T	V	L	12
24	130	H	P	L	R	H	A	T	V	L	12
25	132	L	R	H	A	T	V	L	T	L	12
26	149	A	A	V	V	R	G	A	A	L	12
27	153	R	G	A	A	L	M	A	P	L	12
28	160	P	L	P	V	F	I	K	Q	L	12
29	181	C	L	H	Q	D	V	M	K	L	12
30	182	L	H	Q	D	V	M	K	L	A	12
31	203	I	V	I	I	S	A	I	G	L	12
32	216	I	S	F	S	Y	L	L	I	L	12
33	222	L	I	L	K	T	V	L	G	L	12
34	275	V	I	L	A	N	I	Y	L	L	12
35	37	Y	L	I	A	V	L	G	N	L	11
36	49	Y	I	V	R	T	E	H	S	L	11
37	93	T	I	Q	F	D	A	C	L	L	11
38	101	L	Q	I	F	A	I	H	S	L	11
39	129	C	H	P	L	R	H	A	T	V	11
40	133	R	H	A	T	V	L	T	L	P	11
41	177	S	H	S	Y	C	L	H	Q	D	11
42	207	S	A	I	G	L	D	S	L	L	11
43	257	I	G	L	S	M	V	H	R	F	11

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos		1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L		25
2	268	R	R	D	S	P	L	P	V	I		24
3	132	L	R	H	A	T	V	L	T	L		23

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
4	300	I R Q R I L R L F	23
5	305	L R L F H V A T H	23
6	231	T R E A Q A K A F	21
7	34	C S L Y L I A V L	18
8	299	E I R Q R I L R L	18
9	6	G N E S S A T Y F	17
10	66	C M L S G I D I L	17
11	162	P V F I K Q L P F	17
12	207	S A I G L D S L L	17
13	210	G L D S L L I S F	17
14	220	Y L L I L K T V L	17
15	237	K A F G T C V S H	17
16	269	R D S P L P V I L	17
17	280	I Y L L V P P V L	17
18	295	V K T K E I R Q R	17
19	11	A T Y F I L I G L	16
20	14	F I L I G L P G L	16
21	21	G L E E A Q F W L	16
22	25	A Q F W L A F P L	16
23	37	Y L I A V L G N L	16
24	92	T T I Q F D A C L	16
25	101	L Q I F A I H S L	16
26	124	R Y V A I C H P L	16
27	130	H P L R H A T V L	16
28	141	P R V T K I G V A	16
29	153	R G A A L M A P L	16
30	181	C L H Q D V M K L	16
31	201	G L I V I I S A I	16
32	203	I V I I S A I G L	16
33	216	I S F S Y L L I L	16
34	222	L I L K T V L G L	16
35	255	P F I G L S M V H	16
36	257	I G L S M V H R F	16
37	275	V I L A N I Y L L	16
38	47	I I Y I V R T E H	15
39	109	L S G M E S T V L	15
40	114	S T V L L A M A F	15
41	123	D R Y V A I C H P	15
42	145	K I G V A A V V R	15
43	156	A L M A P L P V F	15
44	168	L P F C R S N I L	15
45	172	R S N I L S H S Y	15
46	198	V V Y G L I V I I	15
47	206	I S A I G L D S L	15
48	229	G L T R E A Q A K	15
49	248	A V F I F Y V P F	15
50	251	I F Y V P F I G L	15
51	274	P V I L A N I Y L	15
52	290	P I V Y G V K T K	15

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
53	298	K E I R Q R I L R	15
54	19	L P G L E E A Q F	14
55	29	L A F P L C S L Y	14
56	30	A F P L C S L Y L	14
57	39	I A V L G N L T I	14
58	40	A V L G N L T I I	14
59	79	S M P K M L A I F	14
60	81	P K M L A I F W F	14
61	99	C L L Q I F A I H	14
62	137	V L T L P R V T K	14
63	138	L T L P R V T K I	14
64	150	A V V R G A A L M	14
65	160	P L P V F I K Q L	14
66	174	N I L S H S Y C L	14
67	180	Y C L H Q D V M K	14
68	192	D D I R V N V V Y	14
69	212	D S L L I S F S Y	14
70	213	S L L I S F S Y L	14
71	214	L L I S F S Y L L	14
72	260	S M V H R F S K R	14
73	263	H R F S K R R D S	14
74	267	K R R D S P L P V	14
75	293	Y G V K T K E I R	14
76	301	R Q R I L R L F H	14
77	302	Q R I L R L F H V	14
78	5	N G N E S S A T Y	13
79	23	E E A Q F W L A F	13
80	28	W L A F P L C S L	13
81	44	N L T I I Y I V R	13
82	51	V R T E H S L H E	13
83	56	S L H E P M Y I F	13
84	60	P M Y I F L C M L	13
85	72	D I L I S T S S M	13
86	74	L I S T S S M P K	13
87	75	I S T S S M P K M	13
88	98	A C L L Q I F A I	13
89	104	F A I H S L S G M	13
90	110	S G M E S T V L L	13
91	116	V L L A M A F D R	13
92	126	V A I C H P L R H	13
93	149	A A V V R G A A L	13
94	158	M A P L P V F I K	13
95	164	F I K Q L P F C R	13
96	170	F C R S N I L S H	13
97	171	C R S N I L S H S	13
98	187	M K L A C D D I R	13
99	217	S F S Y L L I L K	13
100	224	L K T V L G L T R	13
101	242	C V S H V C A V F	13

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
102	256	F	I	G	L	S	M	V	H	R	13
103	261	M	V	H	R	F	S	K	R	R	13
104	49	Y	I	V	R	T	E	H	S	L	12
105	57	L	H	E	P	M	Y	I	F	L	12
106	88	W	F	N	S	T	T	I	Q	F	12
107	96	F	D	A	C	L	L	Q	I	F	12
108	134	H	A	T	V	L	T	L	P	R	12
109	152	V	R	G	A	A	L	M	A	P	12
110	179	S	Y	C	L	H	Q	D	V	M	12
111	197	N	V	V	Y	G	L	I	V	I	12
112	244	S	H	V	C	A	V	F	I	F	12
113	265	F	S	K	R	R	D	S	P	L	12
114	273	L	P	V	I	L	A	N	I	Y	12
115	285	P	P	V	L	N	P	I	V	Y	12
116	288	L	N	P	I	V	Y	G	V	K	12
117	296	K	T	K	E	I	R	Q	R	I	12
118	297	T	K	E	I	R	Q	R	I	L	12

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	24
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	H	A	T	V	L	T	L	22
4	267	K	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	I	L	R	L	F	20
6	231	T	R	E	A	Q	A	K	A	F	19
7	302	Q	R	I	L	R	L	F	H	V	19
8	124	R	Y	V	A	I	C	H	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	I	V	15
11	216	I	S	F	S	Y	L	L	I	L	15
12	11	A	T	Y	F	I	L	I	G	L	14
13	25	A	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	M	A	P	L	14
15	174	N	I	L	S	H	S	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	H	R	F	14
18	280	I	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	A	T	Y	F	13
20	14	F	I	L	I	G	L	P	G	L	13
21	21	G	L	E	E	A	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13
23	130	H	P	L	R	H	A	T	V	L	13
24	201	G	L	I	V	I	I	S	A	I	13
25	203	I	V	I	I	S	A	I	G	L	13

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
26	214	L	L	I	S	F	S	Y	L	L	13
27	251	I	F	Y	V	P	F	I	G	L	13
28	263	H	R	F	S	K	R	R	D	S	13
29	275	V	I	L	A	N	I	Y	L	L	13
30	305	L	R	L	F	H	V	A	T	H	13
31	30	A	F	P	L	C	S	L	Y	L	12
32	34	C	S	L	Y	L	I	A	V	L	12
33	37	Y	L	I	A	V	L	G	N	L	12
34	51	V	R	T	E	H	S	L	H	E	12
35	60	P	M	Y	I	F	L	C	M	L	12
36	75	I	S	T	S	S	M	P	K	M	12
37	93	T	I	Q	F	D	A	C	L	L	12
38	123	D	R	Y	V	A	I	C	H	P	12
39	135	A	T	V	L	T	L	P	R	V	12
40	138	L	T	L	P	R	V	T	K	I	12
41	149	A	A	V	V	R	G	A	A	L	12
42	155	A	A	L	M	A	P	L	P	V	12
43	168	L	P	F	C	R	S	N	I	L	12
44	181	C	L	H	Q	D	V	M	K	L	12
45	188	K	L	A	C	D	D	I	R	V	12
46	190	A	C	D	D	I	R	V	N	V	12
47	195	R	V	N	V	V	Y	G	L	I	12
48	210	G	L	D	S	L	L	I	S	F	12
49	213	S	L	L	I	S	F	S	Y	L	12
50	220	Y	L	L	I	L	K	T	V	L	12
51	248	A	V	F	I	F	Y	V	P	F	12
52	279	N	I	Y	L	L	V	P	P	V	12
53	287	V	L	N	P	I	V	Y	G	V	12
54	296	K	T	K	E	I	R	Q	R	I	12
55	299	E	I	R	Q	R	I	L	R	L	12

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	A	V	L	G	N	L	T	I	26
2	31	F	P	L	C	S	L	Y	L	I	25
3	120	M	A	F	D	R	Y	V	A	I	24
4	130	H	P	L	R	H	A	T	V	L	23
5	118	L	A	M	A	F	D	R	Y	V	22
6	140	L	P	R	V	T	K	I	G	V	22
7	155	A	A	L	M	A	P	L	P	V	22
8	42	L	G	N	L	T	I	I	Y	I	21
9	254	V	P	F	I	G	L	S	M	V	21
10	284	V	P	P	V	L	N	P	I	V	21
11	168	L	P	F	C	R	S	N	I	L	20
12	235	Q	A	K	A	F	G	T	C	V	20
13	138	L	T	L	P	R	V	T	K	I	19

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
14	159	A P L P V F I K Q	18
15	189	L A C D D I R V N	18
16	198	V V Y G L I V I I	18
17	277	L A N I Y L L V P	18
18	207	S A I G L D S L L	17
19	283	L V P P V L N P I	17
20	63	I F L C M L S G I	16
21	86	I F W F N S T T I	16
22	110	S G M E S T V L L	16
23	144	T K I G V A A V V	16
24	149	A A V V R G A A L	16
25	197	N V V Y G L I V I	16
26	271	S P L P V I L A N	16
27	280	I Y L L V P P V L	16
28	3	D P N G N E S S A	15
29	40	A V L G N L T I I	15
30	97	D A C L L Q I F A	15
31	132	L R H A T V L T L	15
32	222	L I L K T V L G L	15
33	279	N I Y L L V P P V	15
34	285	P P V L N P I V Y	15
35	289	N P I V Y G V K T	15
36	9	S S A T Y F I L I	14
37	65	L C M L S G I D I	14
38	84	L A I F W F N S T	14
39	126	V A I C H P L R H	14
40	157	L M A P L P V F I	14
41	158	M A P L P V F I K	14
42	191	C D D I R V N V V	14
43	200	Y G L I V I I S A	14
44	209	I G L D S L L I S	14
45	215	L I S F S Y L L I	14
46	219	S Y L L I L K T V	14
47	220	Y L L I L K T V L	14
48	237	K A F G T C V S H	14
49	247	C A V F I F Y V P	14
50	249	V F I F Y V P F I	14
51	251	I F Y V P F I G L	14
52	257	I G L S M V H R F	14
53	268	R R D S P L P V I	14
54	273	L P V I L A N I Y	14
55	29	L A F P L C S L Y	13
56	33	L C S L Y L I A V	13
57	55	H S L H E P M Y I	13
58	67	M L S G I D I L I	13
59	80	M P K M L A I F W	13
60	95	Q F D A C L L Q I	13
61	98	A C L L Q I F A I	13
62	104	F A I H S L S G M	13

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
63	146	I	G	V	A	A	V	V	R	G	13
64	148	V	A	A	V	V	R	G	A	A	13
65	153	R	G	A	A	L	M	A	P	L	13
66	233	E	A	Q	A	K	A	F	G	T	13
67	243	V	S	H	V	C	A	V	F	I	13
68	292	V	Y	G	V	K	T	K	E	I	13
69	296	K	T	K	E	I	R	Q	R	I	13

Table XXVII, beginning at page 201, line 1, has been amended as follows:

Table XXVII:
HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS
2133-2153, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	D	I	R	V	N	V	V	Y	27
2	244	S	H	V	C	A	V	F	I	F	Y	24
3	40	A	V	L	G	N	L	T	I	I	Y	21
4	284	V	P	P	V	L	N	P	I	V	Y	21
5	116	V	L	L	A	M	A	F	D	R	Y	20
6	28	W	L	A	F	P	L	C	S	L	Y	18
7	297	T	K	E	I	R	Q	R	I	L	R	17
8	21	G	L	E	E	A	Q	F	W	L	A	16
9	22	L	E	E	A	Q	F	W	L	A	F	16
10	52	R	T	E	H	S	L	H	E	P	M	16
11	53	T	E	H	S	L	H	E	P	M	Y	16
12	57	L	H	E	P	M	Y	I	F	L	C	16
13	111	G	M	E	S	T	V	L	L	A	M	16
14	272	P	L	P	V	I	L	A	N	I	Y	16
15	1	M	V	D	P	N	G	N	E	S	S	15
16	4	P	N	G	N	E	S	S	A	T	Y	15
17	121	A	F	D	R	Y	V	A	I	C	H	15
18	171	C	R	S	N	I	L	S	H	S	Y	15
19	211	L	D	S	L	L	I	S	F	S	Y	15
20	8	E	S	S	A	T	Y	F	I	L	I	13
21	190	A	C	D	D	I	R	V	N	V	V	13

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	221	L	L	I	L	K	T	V	L	G	L	30
2	100	L	L	Q	I	F	A	I	H	S	L	29
3	282	L	L	V	P	P	V	L	N	P	I	27
4	205	I	I	S	A	I	G	L	D	S	L	26
5	213	S	L	L	I	S	F	S	Y	L	L	25

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
6	56	S	L	H	E	P	<u>M</u>	Y	I	F	L	24
7	62	Y	I	F	L	C	<u>M</u>	L	S	G	I	24
8	108	S	L	S	G	M	<u>E</u>	S	T	V	L	24
9	117	L	L	A	M	A	<u>F</u>	D	R	Y	V	24
10	131	P	L	R	H	A	<u>T</u>	V	L	T	L	24
11	137	V	L	T	L	P	<u>R</u>	V	T	K	I	24
12	215	L	I	S	F	S	<u>Y</u>	L	L	I	L	24
13	38	L	I	A	V	L	<u>G</u>	N	L	T	I	23
14	41	V	L	G	N	L	<u>T</u>	I	I	Y	I	23
15	156	A	L	M	A	P	<u>L</u>	P	V	F	I	23
16	193	D	I	R	V	N	<u>V</u>	V	Y	G	L	23
17	214	L	L	I	S	F	<u>S</u>	Y	L	L	I	23
18	32	P	L	C	S	L	<u>Y</u>	L	I	A	V	22
19	119	A	M	A	F	D	<u>R</u>	Y	V	A	I	22
20	237	K	A	F	G	T	<u>C</u>	V	S	H	V	22
21	275	V	I	L	A	N	<u>I</u>	Y	L	L	V	22
22	85	A	I	F	W	F	<u>N</u>	S	T	T	I	21
23	139	T	L	P	R	V	<u>T</u>	K	I	G	V	21
24	202	L	I	V	I	I	<u>S</u>	A	I	G	L	21
25	13	Y	F	I	L	I	<u>G</u>	L	P	G	L	20
26	16	L	I	G	L	P	<u>G</u>	L	E	E	A	20
27	29	L	A	F	P	L	<u>C</u>	S	L	Y	L	20
28	142	R	V	T	K	I	<u>G</u>	V	A	A	V	20
29	148	V	A	A	V	V	<u>R</u>	G	A	A	L	20
30	167	Q	L	P	F	C	<u>R</u>	S	N	I	L	20
31	180	Y	C	L	H	Q	<u>D</u>	V	M	K	L	20
32	222	L	I	L	K	T	<u>V</u>	L	G	L	T	20
33	240	G	T	C	V	S	<u>H</u>	V	C	A	V	20
34	248	A	V	F	I	F	<u>Y</u>	V	P	F	I	20
35	250	F	I	F	Y	V	<u>P</u>	F	I	G	L	20
36	271	S	P	L	P	V	<u>I</u>	L	A	N	I	20
37	279	N	I	Y	L	L	<u>V</u>	P	P	V	L	20
38	304	I	L	R	L	F	<u>H</u>	V	A	T	H	20
39	10	S	A	T	Y	F	<u>I</u>	L	I	G	L	19
40	15	I	L	I	G	L	<u>P</u>	G	L	E	E	19
41	27	F	W	L	A	F	<u>P</u>	L	C	S	L	19
42	35	S	L	Y	L	I	<u>A</u>	V	L	G	N	19
43	37	Y	L	I	A	V	<u>L</u>	G	N	L	T	19
44	44	N	L	T	I	I	<u>Y</u>	I	V	R	T	19
45	64	F	L	C	M	L	<u>S</u>	G	I	D	I	19
46	83	M	L	A	I	F	<u>W</u>	F	N	S	T	19
47	159	A	P	L	P	V	<u>F</u>	I	K	Q	L	19
48	189	L	A	C	D	D	<u>I</u>	R	V	N	V	19
49	207	S	A	I	G	L	<u>D</u>	S	L	L	I	19
50	253	Y	V	P	F	I	<u>G</u>	L	S	M	V	19
51	276	I	L	A	N	I	<u>Y</u>	L	L	V	P	19
52	281	Y	L	L	V	P	<u>P</u>	V	L	N	P	19
53	283	L	V	P	P	V	<u>L</u>	N	P	I	V	19
54	286	P	V	L	N	P	<u>I</u>	V	Y	G	V	19
55	33	L	C	S	L	Y	<u>L</u>	I	A	V	L	18

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
56	36	L	Y	L	I	A	V	L	G	N	L	18
57	39	I	A	V	L	G	N	L	T	I	I	18
58	42	L	G	N	L	T	I	I	Y	I	V	18
59	66	C	M	L	S	G	I	D	I	L	I	18
60	111	G	M	E	S	T	V	L	L	A	M	18
61	128	I	C	H	P	L	R	H	A	T	V	18
62	134	H	A	T	V	L	T	L	P	R	V	18
63	154	G	A	A	L	M	A	P	L	P	V	18
64	157	L	M	A	P	L	P	V	F	I	K	18
65	190	A	C	D	D	I	R	V	N	V	V	18
66	229	G	L	T	R	E	A	Q	A	K	A	18
67	245	H	V	C	A	V	F	I	F	Y	V	18
68	274	P	V	I	L	A	N	I	Y	L	L	18
69	278	A	N	I	Y	L	L	V	P	P	V	18
70	291	I	V	Y	G	V	K	T	K	E	I	18
71	298	K	E	I	R	Q	R	I	L	R	L	18
72	48	I	Y	I	V	R	T	E	H	S	L	17
73	65	L	C	M	L	S	G	I	D	I	L	17
74	67	M	L	S	G	I	D	I	L	I	S	17
75	74	L	I	S	T	S	S	M	P	K	M	17
76	91	S	T	T	I	Q	F	D	A	C	L	17
77	94	I	Q	F	D	A	C	L	L	Q	I	17
78	188	K	L	A	C	D	D	I	R	V	N	17
79	197	N	V	V	Y	G	L	I	V	I	I	17
80	200	Y	G	L	I	V	I	I	S	A	I	17
81	218	F	S	Y	L	L	I	L	K	T	V	17
82	227	V	L	G	L	T	R	E	A	Q	A	17
83	303	R	I	L	R	L	F	H	V	A	T	17
84	21	G	L	E	E	A	Q	F	W	L	A	16
85	92	T	T	I	Q	F	D	A	C	L	L	16
86	97	D	A	C	L	L	Q	I	F	A	I	16
87	127	A	I	C	H	P	L	R	H	A	T	16
88	143	V	T	K	I	G	V	A	A	V	V	16
89	195	R	V	N	V	V	Y	G	L	I	V	16
90	220	Y	L	L	I	L	K	T	V	L	G	16
91	296	K	T	K	E	I	R	Q	R	I	L	16
92	18	G	L	P	G	L	E	E	A	Q	F	15
93	30	A	F	P	L	C	S	L	Y	L	I	15
94	126	V	A	I	C	H	P	L	R	H	A	15
95	145	K	I	G	V	A	A	V	V	R	G	15
96	173	S	N	I	L	S	H	S	Y	C	L	15
97	201	G	L	I	V	I	I	S	A	I	G	15
98	208	A	I	G	L	D	S	L	L	I	S	15
99	210	G	L	D	S	L	I	I	S	F	S	15
100	267	K	R	R	D	S	P	L	P	V	I	15

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
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HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
1 141	P	<u>R</u>	V	T	K	I	<u>G</u>	V	A	A	19
2 147	G	<u>V</u>	A	A	V	V	<u>R</u>	G	A	A	19
3 112	M	<u>E</u>	S	T	V	L	<u>L</u>	A	M	A	18
4 227	V	<u>L</u>	<u>G</u>	L	T	R	<u>E</u>	A	Q	A	18
5 229	G	<u>L</u>	T	R	E	A	<u>Q</u>	A	K	A	18
6 142	R	<u>V</u>	T	K	I	<u>G</u>	V	A	A	V	17
7 148	V	<u>A</u>	A	V	V	R	<u>G</u>	A	A	L	17
8 2	V	<u>D</u>	P	N	G	N	<u>E</u>	S	S	A	10
9 16	L	<u>I</u>	<u>G</u>	L	P	<u>G</u>	L	E	E	A	10
10 21	G	<u>L</u>	E	E	A	Q	F	W	L	A	10
11 31	F	<u>P</u>	L	C	S	L	<u>Y</u>	L	I	A	10
12 76	S	<u>T</u>	S	S	M	P	K	M	L	A	10
13 89	F	<u>N</u>	S	T	T	I	<u>Q</u>	F	D	A	10
14 96	F	<u>D</u>	A	C	L	L	<u>Q</u>	I	F	A	10
15 110	S	<u>G</u>	M	E	S	T	V	L	L	A	10
16 118	L	<u>A</u>	M	A	F	D	R	Y	V	A	10
17 126	V	<u>A</u>	I	C	H	P	L	R	H	A	10
18 140	L	<u>P</u>	R	V	T	K	<u>I</u>	G	V	A	10
19 146	I	<u>G</u>	V	A	A	V	V	R	G	A	10
20 150	A	V	V	R	G	A	<u>A</u>	L	M	A	10
21 181	C	<u>L</u>	H	Q	D	V	M	K	L	A	10
22 199	V	<u>Y</u>	<u>G</u>	L	I	V	<u>I</u>	I	S	A	10
23 225	K	<u>T</u>	V	L	<u>G</u>	L	T	R	E	A	10
24 239	F	<u>G</u>	T	C	V	S	H	V	C	A	10
25 269	R	<u>D</u>	S	P	L	P	<u>V</u>	I	L	A	10
26 302	Q	<u>R</u>	I	L	R	L	<u>F</u>	H	V	A	10
27 305	L	<u>R</u>	L	F	H	V	<u>A</u>	T	H	A	10
28 3	D	P	N	G	N	E	S	S	A	T	9
29 17	I	<u>G</u>	L	P	<u>G</u>	L	E	E	A	Q	9
30 22	L	<u>E</u>	E	A	Q	F	W	L	A	F	9
31 32	P	<u>L</u>	C	S	L	<u>Y</u>	L	I	A	V	9
32 77	T	<u>S</u>	S	M	P	K	M	L	A	I	9
33 90	N	<u>S</u>	T	T	I	Q	F	D	A	C	9
34 97	D	<u>A</u>	C	L	L	<u>Q</u>	I	F	A	I	9
35 111	G	<u>M</u>	E	S	T	V	<u>L</u>	L	A	M	9
36 113	E	<u>S</u>	T	V	L	L	<u>A</u>	M	A	F	9
37 119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	I	9
38 127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	T	9
39 151	V	<u>V</u>	R	G	A	<u>A</u>	L	M	A	P	9
40 182	L	H	Q	D	V	M	K	L	A	C	9
41 200	Y	<u>G</u>	L	I	V	<u>I</u>	I	S	A	I	9
42 226	T	<u>V</u>	L	<u>G</u>	L	T	R	E	A	Q	9
43 228	L	<u>G</u>	L	T	R	E	<u>A</u>	Q	A	K	9
44 230	L	T	R	E	A	Q	<u>A</u>	K	A	F	9
45 240	G	<u>T</u>	C	V	S	H	<u>V</u>	C	A	V	9
46 270	D	<u>S</u>	P	L	P	<u>V</u>	I	L	A	N	9
47 303	R	<u>I</u>	L	R	L	<u>F</u>	H	V	A	T	9
48 306	R	<u>L</u>	F	H	V	<u>A</u>	T	H	A	S	9

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	V	L	T	L	P	R	V	T	K	31
2	287	V	L	N	P	I	V	Y	G	V	K	28
3	223	I	L	K	T	V	L	G	L	T	R	27
4	304	I	L	R	L	F	H	V	A	T	H	27
5	73	I	L	I	S	T	S	S	M	P	K	26
6	15	I	L	I	G	L	P	G	L	E	E	23
7	40	A	V	L	G	N	L	T	I	I	Y	23
8	150	A	V	V	R	G	A	A	L	M	A	23
9	258	G	L	S	M	V	H	R	F	S	K	23
10	18	G	L	P	G	L	E	E	A	Q	F	22
11	303	R	I	L	R	L	F	H	V	A	T	22
12	276	I	L	A	N	I	Y	L	L	V	P	21
13	28	W	L	A	F	P	L	C	S	L	Y	20
14	115	T	V	L	L	A	M	A	F	D	R	20
15	116	V	L	L	A	M	A	F	D	R	Y	20
16	125	Y	V	A	I	C	H	P	L	R	H	20
17	131	P	L	R	H	A	T	V	L	T	L	20
18	144	T	K	I	G	V	A	A	V	V	R	20
19	156	A	L	M	A	P	L	P	V	F	I	20
20	195	R	V	N	V	V	Y	G	L	I	V	20
21	35	S	L	Y	L	I	A	V	L	G	N	19
22	272	P	L	P	V	I	L	A	N	I	Y	19
23	37	Y	L	I	A	V	L	G	N	L	T	18
24	49	Y	I	V	R	T	E	H	S	L	H	18
25	50	I	V	R	T	E	H	S	L	H	E	18
26	108	S	L	S	G	M	E	S	T	V	L	18
27	142	R	V	T	K	I	G	V	A	A	V	18
28	188	K	L	A	C	D	D	I	R	V	N	18
29	279	N	I	Y	L	L	V	P	P	V	L	18
30	291	I	V	Y	G	V	K	T	K	E	I	18

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
31	294	G	V	<u>K</u>	T	<u>K</u>	<u>E</u>	<u>I</u>	R	Q	R	18
32	46	T	<u>I</u>	<u>I</u>	Y	I	<u>V</u>	<u>R</u>	T	E	H	17
33	102	Q	<u>I</u>	<u>F</u>	A	<u>I</u>	<u>H</u>	<u>S</u>	L	S	G	17
34	151	V	<u>V</u>	<u>R</u>	G	A	<u>A</u>	<u>L</u>	M	A	P	17
35	179	S	<u>Y</u>	<u>C</u>	L	H	<u>Q</u>	<u>D</u>	V	M	K	17
36	203	I	<u>V</u>	<u>I</u>	I	S	A	<u>I</u>	G	L	D	17
37	204	V	<u>I</u>	<u>I</u>	S	A	<u>I</u>	<u>G</u>	L	D	S	17
38	220	Y	<u>L</u>	<u>L</u>	I	L	<u>K</u>	<u>T</u>	V	L	G	17
39	221	L	<u>L</u>	<u>I</u>	L	<u>K</u>	<u>T</u>	V	L	G	L	17
40	227	V	<u>L</u>	<u>G</u>	L	T	<u>R</u>	<u>E</u>	A	Q	A	17
41	242	C	<u>V</u>	<u>S</u>	H	V	<u>C</u>	A	V	F	I	17
42	289	N	<u>P</u>	<u>I</u>	V	Y	G	V	K	T	K	17
43	38	L	<u>I</u>	<u>A</u>	V	L	<u>G</u>	<u>N</u>	L	T	I	16
44	85	A	<u>I</u>	<u>F</u>	W	F	<u>N</u>	<u>S</u>	T	T	I	16
45	147	G	<u>V</u>	<u>A</u>	A	V	<u>V</u>	<u>R</u>	G	A	A	16
46	198	V	<u>V</u>	<u>Y</u>	G	L	<u>I</u>	V	I	I	S	16
47	201	G	<u>L</u>	<u>I</u>	V	I	<u>I</u>	S	A	I	G	16
48	214	L	<u>L</u>	<u>I</u>	S	F	<u>S</u>	<u>Y</u>	L	L	I	16
49	226	T	<u>V</u>	<u>L</u>	G	L	T	<u>R</u>	E	A	Q	16
50	228	L	<u>G</u>	<u>L</u>	T	<u>R</u>	<u>E</u>	A	Q	A	K	16
51	229	G	<u>L</u>	T	<u>R</u>	<u>E</u>	A	Q	A	K	A	16
52	1	M	<u>V</u>	<u>D</u>	P	N	<u>G</u>	<u>N</u>	E	S	S	15
53	44	N	<u>L</u>	T	I	I	Y	I	V	R	T	15
54	47	I	<u>I</u>	<u>Y</u>	I	V	<u>R</u>	T	E	H	S	15
55	67	M	<u>L</u>	<u>S</u>	G	I	<u>D</u>	<u>I</u>	L	I	S	15
56	72	D	<u>I</u>	<u>L</u>	I	S	T	<u>S</u>	S	M	P	15
57	99	C	<u>L</u>	<u>L</u>	Q	I	<u>F</u>	A	I	H	S	15
58	105	A	<u>I</u>	<u>H</u>	S	L	<u>S</u>	G	M	E	S	15
59	145	K	<u>I</u>	<u>G</u>	V	A	A	V	V	R	G	15
60	175	I	<u>L</u>	<u>S</u>	H	S	<u>Y</u>	<u>C</u>	L	H	Q	15
61	191	C	<u>D</u>	<u>D</u>	I	R	<u>V</u>	<u>N</u>	V	V	Y	15
62	208	A	<u>I</u>	<u>G</u>	L	D	<u>S</u>	<u>L</u>	L	I	S	15
63	275	V	<u>I</u>	<u>L</u>	A	N	<u>I</u>	<u>Y</u>	L	L	V	15
64	281	Y	<u>L</u>	<u>L</u>	V	P	P	V	L	N	P	15
65	299	E	<u>I</u>	<u>R</u>	Q	R	<u>I</u>	<u>L</u>	R	L	F	15
66	306	R	<u>L</u>	<u>F</u>	H	V	<u>A</u>	T	H	A	S	15

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	159	A	<u>P</u>	<u>L</u>	P	V	F	I	K	Q	L	23
2	59	E	<u>P</u>	<u>M</u>	Y	I	F	L	C	M	L	22
3	273	L	<u>P</u>	<u>V</u>	I	L	A	N	I	Y	L	20
4	3	D	<u>P</u>	<u>N</u>	G	N	E	S	S	A	T	19
5	130	H	<u>P</u>	<u>L</u>	R	H	A	T	V	L	T	19
6	140	L	<u>P</u>	<u>R</u>	V	T	K	I	G	V	A	19
7	161	L	<u>P</u>	<u>V</u>	F	I	K	Q	L	P	F	19
8	31	F	<u>P</u>	<u>L</u>	C	S	L	Y	L	I	A	18
9	271	S	<u>P</u>	<u>L</u>	P	V	I	L	A	N	I	18

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
10	80	M	P	K	M	L	A	I	F	W	F	16
11	108	S	L	S	G	M	E	S	T	V	L	16
12	131	P	L	R	H	A	T	V	L	T	L	15
13	264	R	F	S	K	R	R	D	S	P	L	15
14	33	L	C	S	L	Y	L	I	A	V	L	14
15	109	L	S	G	M	E	S	T	V	L	L	14
16	152	V	R	G	A	A	L	M	A	P	L	14
17	205	I	I	S	A	I	G	L	D	S	L	14
18	215	L	I	S	F	S	Y	L	L	I	L	14
19	268	R	R	D	S	P	L	P	V	I	L	14
20	29	L	A	F	P	L	C	S	L	Y	L	13
21	148	V	A	A	V	V	R	G	A	A	L	13
22	156	A	L	M	A	P	L	P	V	F	I	13
23	193	D	I	R	V	N	V	V	Y	G	L	13
24	221	L	L	I	L	K	T	V	L	G	L	13
25	298	K	E	I	R	Q	R	I	L	R	L	13
26	7	N	E	S	S	A	T	Y	F	I	L	12
27	19	L	P	G	L	E	E	A	Q	F	W	12
28	24	E	A	Q	F	W	L	A	F	P	L	12
29	119	A	M	A	F	D	R	Y	V	A	I	12
30	129	C	H	P	L	R	H	A	T	V	L	12
31	206	I	S	A	I	G	L	D	S	L	L	12
32	219	S	Y	L	L	I	L	K	T	V	L	12
33	279	N	I	Y	L	L	V	P	P	V	L	12
34	285	P	P	V	L	N	P	I	V	Y	G	12
35	8	E	S	S	A	T	Y	F	I	L	I	11
36	13	Y	F	I	L	I	G	L	P	G	L	11
37	27	F	W	L	A	F	P	L	C	S	L	11
38	48	I	Y	I	V	R	T	E	H	S	L	11
39	56	S	L	H	E	P	M	Y	I	F	L	11
40	65	L	C	M	L	S	G	I	D	I	L	11
41	75	I	S	T	S	S	M	P	K	M	L	11
42	77	T	S	S	M	P	K	M	L	A	I	11
43	91	S	T	T	I	Q	F	D	A	C	L	11
44	123	D	R	Y	V	A	I	C	H	P	L	11
45	142	R	V	T	K	I	G	V	A	A	V	11
46	180	Y	C	L	H	Q	D	V	M	K	L	11
47	190	A	C	D	D	I	R	V	N	V	V	11
48	212	D	S	L	L	I	S	F	S	Y	L	11
49	234	A	Q	A	K	A	F	G	T	C	V	11
50	242	C	V	S	H	V	C	A	V	F	I	11
51	248	A	V	F	I	F	Y	V	P	F	I	11
52	250	F	I	F	Y	V	P	F	I	G	L	11
53	254	V	P	F	I	G	L	S	M	V	H	11
54	266	S	K	R	R	D	S	P	L	P	V	11
55	267	K	R	R	D	S	P	L	P	V	I	11
56	269	R	D	S	P	L	P	V	I	L	A	11
57	278	A	N	I	Y	L	L	V	P	P	V	11
58	284	V	P	P	V	L	N	P	I	V	Y	11
59	289	N	P	I	V	Y	G	V	K	T	K	11

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
60 296	K	T	K	E	I	R	Q	R	I	L	11

Table XXVIII, beginning at page 205, line 1, has been amended as follows:

Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)
HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	36
2 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	34
3 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	33
4 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	32
5 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	31
6 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	31
7 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	31
8 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	30
9 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	30
10 240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	30
11 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	29
12 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	29
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	28
14 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	27
15 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	26
16 183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	26
17 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	26
18 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	25
19 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	25
20 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	25
21 70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	25
22 111	G	M	E	S	T	V	L	L	A	M	A	F	D	R	Y	25
23 148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	25
24 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	25
25 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	25
26 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	25
27 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	25
28 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	24
29 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	24
30 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	24
31 77	T	S	S	M	P	K	M	L	A	I	F	W	F	N	S	24
32 85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	24
33 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	24
34 151	V	V	R	G	A	A	L	M	A	P	L	P	V	F	I	24
35 161	L	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	24
36 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	24

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
37	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	24
38	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	24
39	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	24
40	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	24
41	83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	23
42	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	23
43	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	23
44	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	23
45	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	23
46	278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	23
47	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	22
48	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	22
49	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	22
50	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	22
51	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	22
52	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	22
53	146	I	G	V	A	A	V	V	R	G	A	A	L	M	A	P	22
54	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	22
55	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	22
56	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	22
57	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	22
58	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	22
59	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	22
60	34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	21
61	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	21
62	152	V	R	G	A	A	L	M	A	P	L	P	V	F	I	K	21
63	299	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	H	21
64	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
65	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	20
66	141	P	R	V	T	K	I	G	V	A	A	V	V	R	G	A	20
67	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	20
68	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
69	262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	20
70	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	20
71	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	19
72	58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	19
73	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	19
74	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	19
75	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	19
76	215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	19
77	219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	19
78	228	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	19
79	232	R	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	19
80	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	19
81	297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	19
82	3	D	P	N	G	N	E	S	S	A	T	Y	F	I	L	I	18
83	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	18
84	25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	18
85	42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	18
86	46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	18
87	78	S	S	M	P	K	M	L	A	I	F	W	F	N	S	T	18

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
88	84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	18
89	89	F	N	S	T	T	I	Q	F	D	A	C	L	L	Q	I	18
90	93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
91	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	18
92	119	A	M	A	F	D	R	Y	V	A	I	C	H	P	L	R	18
93	127	A	I	C	H	P	L	R	H	A	T	V	L	T	L	P	18
94	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	18
95	147	G	V	A	A	V	V	R	G	A	A	L	M	A	P	L	18
96	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	18
97	216	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	18
98	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	18
99	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
100	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	18
101	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	18
102	286	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	I	18
103	303	R	I	L	R	L	F	H	V	A	T	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	26
2	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	23
3	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	22
4	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	22
5	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	21
6	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	21
7	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	21
8	219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	21
9	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	21
10	26	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	20
11	114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	20
12	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
13	134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
14	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
15	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
16	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	20
17	297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	20
18	11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	19
19	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	19
20	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	19
21	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	19
22	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	19
23	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	19
24	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	19
25	224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	19
26	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	19
27	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	19
28	254	V	P	F	I	G	L	S	M	V	H	R	F	S	K	R	19
29	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	19

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
30	36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	18
31	93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
32	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	18
33	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	18
34	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	18
35	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
36	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	18
37	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	18
38	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	18
39	288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	18
40	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	17
41	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	17
42	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	17
43	159	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	17
45	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
46	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	16
47	262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	16
48	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49	46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	15
50	51	V	R	T	E	H	S	L	H	E	P	M	Y	I	F	L	15
51	172	R	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	15
52	189	L	A	C	D	D	I	R	V	N	V	V	Y	G	L	I	15
53	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	15
54	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	15
55	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	15
56	279	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	15
57	12	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	14
58	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	14
59	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
60	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
61	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
62	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	14
63	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	13
64	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	13
65	71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	13
66	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	13
67	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13
69	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	13
70	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	13
71	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	13
72	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	13
73	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	13
74	264	R	F	S	K	R	R	D	S	P	L	P	V	I	L	A	13
75	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	13
76	302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers
 (SEQ ID NOS 2672-2805, respectively
 in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	26
2	45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	26
3	68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	26
4	83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	26
5	134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	26
6	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	26
7	224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	26
8	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	26
9	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	26
10	281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	26
11	289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	26
12	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	26
13	11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	22
14	24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	22
15	25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	22
16	34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	22
17	84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	22
18	122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	22
19	197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	22
20	215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	22
21	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	22
22	250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	22
23	278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	22
24	19	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	L	20
25	30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	20
26	33	L	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	20
27	35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	20
28	39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	20
29	42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	20
30	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	20
31	48	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	Y	20
32	58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	20
33	62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	20
34	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	20
35	71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	20
36	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	20
37	81	P	K	M	L	A	I	F	W	F	N	S	T	T	I	Q	20
38	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	20
39	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	20
40	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	20
41	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
42	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	20
43	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	20
44	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	20
45	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	20
46	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	20
47	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
48	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
49	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	20

HLA-DRB1*0401 (DR4Dw4) 15-mers
 (SEQ ID NOS 2672-2805, respectively
 in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	20
57	196	V	N	V	Y	G	L	I	V	I	I	S	A	I	G	L	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16

HLA-DRB1*0401 (DR4Dw4) 15-mers
 (SEQ ID NOS 2672-2805, respectively
 in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
99	236	A	K	A	F	G	T	C	V	S	H	V	C	A	V	F	16
100	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	16
101	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	14
105	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	14
106	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	14
107	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	14
108	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	14
109	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
110	70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	14
111	72	D	I	L	I	S	T	S	S	M	P	K	M	L	A	I	14
112	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	14
113	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	14
114	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	14
115	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	14
116	148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	14
117	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	14
118	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	14
119	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	M	14
121	184	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	V	14
122	191	C	D	D	I	R	V	N	V	Y	G	L	I	V	I	I	14
123	195	R	V	N	V	Y	G	L	I	V	I	I	S	A	I		14
124	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	14
126	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	14
127	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	14
129	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	14
133	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	14
134	302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
 (SEQ ID NOS 2806-2866, respectively
 in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score	
1	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	28
2	122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	25
3	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	25
4	197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	24
5	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	23
6	255	P	F	I	G	L	S	M	V	H	R	F	S	K	R	R	23
7	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	22

HLA-DRB1*1101 15-mers
 (SEQ ID NOS 2806-2866, respectively
 in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
8 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	22
10 237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	22
11 74	L	I	S	T	S	S	M	P	K	M	L	A	I	F	W	21
12 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
13 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
14 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
15 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
16 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	20
17 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18 290	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	I	20
19 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	19
22 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	19
23 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	19
24 247	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	19
25 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	19
26 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	18
27 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	18
28 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	18
29 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	18
30 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	18
32 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
33 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	17
34 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	17
35 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
36 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	17
37 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	17
38 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	16
39 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	16
40 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	16
41 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
42 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	15
43 99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	15
44 116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	15
45 143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	15
46 179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	15
47 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	15
48 260	S	M	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49 261	M	V	H	R	F	S	K	R	R	D	S	P	L	P	V	15
50 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	15
51 285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	15
52 114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	14
53 125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	14
54 126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	14
55 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
56 170	F	C	R	S	N	I	L	S	H	S	Y	C	L	H	Q	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
57 180	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	I	14
58 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	14
59 229	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	V	14
60 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
61 298	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	14

Table XXIX, beginning at page 213, line 1, has been amended as follows:

Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

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1  TGCCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTAAATA GAGGCAGGGT TTCACCATGT
61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GGCAGGGCTT ATTGTTTTTT AAAAAGATTT
181 CAAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
241 TGTTGTCAAT TACTTTAGAT GTTCTATCA GGAAAGTTT AGAAATGGTA TTCAGGCCTA
301 AACACAAACC TCTCTTGAAT TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCATGGGA
601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTCTACTTT TTCCCTTTCT ACTTTCTTAG
841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCATTGT CCTCATCATT CGTGTGGAGA GGCAGCTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCTT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG GTGCTCTGCT GGCCATGGCT TTTGACCGCT
1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTCACACA CTCCTTCTGT CTGCACCAAG
1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGCACTCAA GGCTTTCAAC ACCTGCATCT
1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
1741 CACCTGTAGT CAACCCCTTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
1921 TTGTGCTGTC TTCTTCCAGC AATTAAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
1981 AGTATGCAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACCTA GTCCCTCTGC
2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT

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2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
2221 CCTAAAGTGG TTACCCAGCC ATAATCAGGG GTTAATGAAG GTATTTGGGG AATAGTAACT
2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT CTGTATGCAA
2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGCACA CATGGAATAC
2521 GTACTGGTTG TGTCCCTGGT AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
2581 ACGTGTCTCT GATTGCGCAT TTGTATTTCT GTGGTATCTG TTAGTTGGTA TATGATATGT
2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
2701 GGTAAGAATG CTGCCTCTAC CTTTTCTTCC TATTTGTACT ATGTGAATGT GGTGCATGAA
2761 TGTGTGGAAT GTGTGGAATG TGTAGTATTG GGATGCCCTG ATCTTTTCAGC GTGTTTGGGT
2821 GTATGTCCAC TGTGCATAAT ATTTGAGATG TAAACCATT TTGTGCGGTA TATGTGTTAT
2881 TAGTTGTAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG TACTGATGC
2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTAAAGGCAA ACTTTCCTTG TGTGTTGGGT
3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTCTCGGC CTGGGGTCAG
3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
3241 TTTCACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGTT
3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCTCCCTA AACCTGCCC
3361 TCCTGCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTTT GGCTTATCTG
3421 CCAAACATGT ATAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAAC AATTAGCCCG
3481 GTGTGATGGC GCGTGCCCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCTTCTGTT
3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAGCATTC ACCTCATTAT
3781 TCACCTTGTC TCATGTCTCA CTGTCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
3841 GAAGTAGAAG TCCCTTTGGT ATTTTTTAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTCAGGCTG CGTGCTCTGT
3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAACT
4081 CACAGTTGTG AAACTGATCA GTAAAAATA AGGGGGAGACC AACTAAAAAC CATGTTGTTT
4141 TATTTATAGA TGTAGTTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTG CCCTTAAGGG AGAAACCAGA
4261 TGTCATTGGT CTTACGTGGC TGGTGTGGG GGTGGGAGG GTTAAAGAAA CCACGTTCTC
4321 TGTCTCAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCACGTGTC
4381 CTGGGGACCT TGGTTATAAG TTATCCAGAC ACAGGGACCA GAGCCTGGGA GACAAAAAAA
4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTTCCA CGCTTAGCAA
4501 GGACCTAAAC AGTGTCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
4561 AAATGGGCTG AACTTAACC GTGGAGTGTC TCTGCAACT TCCTTTGCCA TTCTCCTGTT
4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
4681 AGTTTCTTCT AGCTTTTTTC TACTACTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
4741 ATGAGGATCC CAGCAGCCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTGCCTCT
4801 CCTCCCCATA CCCCAGGCA TATCCTCCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCATT CTGCCCCACC
4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TGAGGCAGAG AATAAATAAC CCTGACCAGG
4981 GAGGTCCAAG GGAGTAGGCG GAGAcagaga ggctgtattt cagtgcagcc tgccagacct

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Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.

Table XXX, beginning at page 214, line 35, has been amended as follows

Query: 202 caagctcgcctcctgggttcacgccatttctcctgcctcagcctcctgagttagctgggac 261
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 3561 caacctccacttgcggtcgaagcgtttctcctgcctcagcctcccactagctgggac 3502

NF-1

```
Query: 262  tacaggcacccgcccaccacgcctggttaannnnnnngtatttttagtagagatgggg 318
          ||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 3501  tacaggcacgcgcccatcacaccggctaa--ttgttgatttttagtagagatgggg 3447
```

4.
Query: 300 attttagtagagatgggggtttcactgtgttagccaggatgggtctcagtcctctgacctc 359
(SEQ ID NO: 2874)

Sbjct: 31 atttttaatatagaggcaggggttcaccatgttggcctggctggtctcgaaccctgacctt 90
(SEQ ID NO: 2875)

		<u>SP1</u>		<u>NF-1</u>	
		<u>LF-A1</u>		<u>CP2</u>	
Query:	360	gtgatctgcccaccttggcctcccaaagtgctgggattacaggcgctgagccactg	g	gcgcct	419
Sbjct:	91	gcgatctgcccacctcgccctcccaaagtgctgggattacaggcgctgagccactgt	a	tacct	150

```

      NF-1
Query: 420 ggc 422
      |||
Sbjct: 151 ggc 153

```

5. NF-1 CP2

Query: 4506 gccaggcacagtggtctcacgcctgtaatcccaacacccatgggaggctgagatgggtggat 4565

(SEQ ID NO: 2876)

|||||

Sbjct: 153 gccaggtacagtggtctcacgcctgtaatcccagcactttgggaggccgaggtgggcagat 94

(SEQ ID NO: 2877)

Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 93 cgcaaggtcaggggttcgagaccagccaggccaacatggtgaaacctgcctcta 39

Figure 1 (SEQ ID NO:2878)

GATCAAACTTCTTTCCATTGAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTGGAAGACAGTATTCAGAAAAAAATTTCC
TTAATAAAAAATACAACTCAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTCTTCTTTGTTTTT
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTGGATC

FIG. 2A (SEQ ID NOS:2879 & 2880)

5' CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 63 72 81 90 99 108
 ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 117 126 135 144 153 162
 TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M M V D P N G N E S S
 171 180 189 198 207 216
 GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A T Y F I L I G L P G L E E A Q F W
 225 234 243 252 261 270
 TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L A F P L C S L Y L I A V L G N L T
 279 288 297 306 315 324
 ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I I Y I V R T E H S L H E P M Y I F
 333 342 351 360 369 378
 CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L C M L S G I D I L I S T S S M P K
 387 396 405 414 423 432
 ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M L A I F W F N S T T I Q F D A C L
 441 450 459 468 477 486
 CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L Q I F A I H S L S G M E S T V L L
 495 504 513 522 531 540
 GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A M A F D R Y V A I C H P L R H A T
 549 558 567 576 585 594
 GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V L T L P R V T K I G V A A V V R G
 603 612 621 630 639 648
 GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A A L M A P L P V F I K Q L P F C R

FIG. 2B

657	666	675	684	693	702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC					
S N I L S H S Y C L H Q D V M K L A					
711	720	729	738	747	756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC					
C D D I R V N V V Y G L I V I I S A					
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT					
I G L D S L L I S F S Y L L I L K T					
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT					
V L G L T R E A Q A K A F G T C V S					
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG					
H V C A V F I F Y V P F I G L S M V					
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC					
H R F S K R R D S P L P V I L A N I					
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG					
Y L L V P P V L N P I V Y G V K T K					
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG					
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT					
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA					
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT					
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC					
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA					

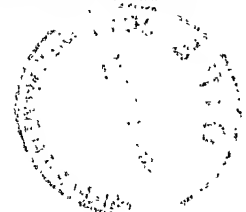


FIG. 2C

1359	1368	1377	1386	1395	1404
AAC TGC TTC	TAC TGA TGG	TTT ACA GCA	TTC TGA GAT	AAG AAT GGT	ACA TCT AGA
1413	1422	1431	1440	1449	1458
GAA CAT TTG	CCA AAG GCC	TAA GCA CGG	CAA AGG AAA	ATA AAC ACA	GAA TAT AAT
1467	1476	1485	1494	1503	1512
AAA ATG AGA	TAA TCT AGC	TTA AAA CTA	TAA CTT CCT	CTT CAG AAC	TCC CAA CCA
1521	1530	1539	1548	1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT CTT	CAA AAT GAC	TTC TAC AGA	GAA GAA ATA
1575	1584	1593	1602	1611	1620
ATT TTT CCT	CTG GAC ACT	AGC ACT TAA	GGG GAA GAT	TGG AAG TAA	AGC CTT GAA
1629	1638	1647	1656	1665	1674
AAG AGT ACA	TTT ACC TAC	GTT AAT GAA	AGT TGA CAC	ACT GTT CTG	AGA GTT TTC
1683	1692	1701	1710	1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC TAT	TTA ATT TTC	TTA TCA ACC	CTT TAA TTA
1737	1746	1755	1764	1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC ATT	GTA GCC ATG	GGA AAA TTG	ATG TTC AGT
1791	1800	1809	1818	1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT CAT	ACA AGT ATA	AAA ATT AAA	AAA AAA AAA
1845	1854	1863	1872	1881	1890
GAC TTC ATG	CCC AAT CTC	ATA TGA TGT	GGA AGA ACT	GTT AGA GAG	ACC AAC AGG
1899	1908	1917	1926	1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG TCT	TAC ATT TTC	TAG AGG AGG	TAT TTA ATT
1953	1962	1971	1980	1989	1998
TCT TCT CAC	TCA TCC AGT	GTT GTA TTT	AGG AAT TTC	CTG GCA ACA	GAA CTC ATG
2007	2016	2025	2034	2043	2052
GCT TTA ATC	CCA CTA GCT	ATT GCT TAT	TGT CCT GGT	CCA ATT GCC	AAT TAC CTG
2061	2070	2079	2088	2097	2106
TGT CTT GGA	AGA AGT GAT	TTC TAG GTT	CAC CAT TAT	GGA AGA TTC	TTA TTC AGA
2115	2124	2133	2142	2151	2160
AAG TCT GCA	TAG GGC TTA	TAG CAA GTT	ATT TAT TTT	TAA AAG TTC	CAT AGG TGA
2169	2178	2187	2196	2205	2214
TTC TGA TAG	GCA GTG AGG	TTA GGG AGC	CAC CAG TTA	TGA TGG GAA	GTA TGG AAT
2223	2232	2241	2250	2259	2268
GGC AGG TCT	TGA AGA TAA	CAT TGG CCT	TTT GAG TGT	GAC TCG TAG	CTG GAA AGT
2277	2286	2295	2304	2313	2322
GAG GGA ATC	TTC AGG ACC	ATG CTT TAT	TTG GGG CTT	TGT GCA GTA	TGG AAC AGG
2331	2340	2349	2358	2367	2376
GAC TTT GAG	ACC AGG AAA	GCA ATC TGA	CTT AGG CAT	GGG AAT CAG	GCA TTT TTG

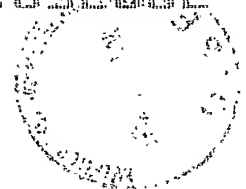


FIG. 2D

2385	2394	2403	2412	2421	2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA					
2439	2448	2457	2466	2475	2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT					
2493	2502	2511	2520	2529	2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC					
2547	2556	2565	2574	2583	2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT					
2601	2610	2619	2628	2637	2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT					
2655	2664	2673	2682	2691	2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC					
2709	2718	2727	2736	2745	2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT					
2763	2772	2781	2790	2799	2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT					
2817	2826	2835	2844	2853	2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA					
2871	2880	2889	2898	2907	2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT					
2925	2934	2943	2952	2961	2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG					
2979	2988	2997	3006	3015	3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT					
3033	3042	3051	3060	3069	3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT					
3087	3096	3105	3114	3123	3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA					

AAA A 3'

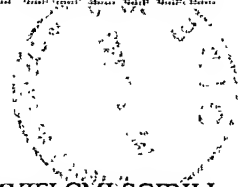


Figure 3: Protein Sequence for 101P3A11 (piece of SEQ ID NO:2880)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG
VKTKEIRQRILRLFHVATHASEP



Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

Query: 34 GNYTVVTEFILLGLTDDITVSVILFVMFLIVSVTLMGNLNIIIVLIRTSPQLHTPMYLF 93
 GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL

Sbjct: 6 GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94 SHLAFLDIGYSSSVTPIMLRGFLRKGTFFIPVAGCVAQLCIVVAFGTSESFLLASMAVDY 153
 L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY

Sbjct: 66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGWVNAWIFTGCSLNL SFCGPNKINHFFCDYSP 213
 VAIC PL ++T ++ + + + G L FC N ++H +C +

Sbjct: 126 VAICHPLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCSRNL SHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISGSIIVTVFIIALSYYVILVSILKMRSTEGRQKAFSTCTS 273
 ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S

Sbjct: 186 VMKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
 H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++

Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRDRSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQ 302

Query: 330 AMKKL 334 (SEQ ID NO:2881)
 + +L

Sbjct: 303 RILRL 307 (SEQ ID NO:2882)



Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

```

PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
        F+LIG+PGLEEA FW  FPL S+Y +A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
RA1C: 11  FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERS LHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
        +STS+MPK+LA+FWF+S  I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
RA1C: 71  ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTVKIGVAAVVRGAALMAPLVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
        HA VL      +IG+ A+VRG+  PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
RA1C: 131 HAAVLNNTVTTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
        NVVYGL  I+  +G+D + IS SY LI++ VL L ++  +AKAFGTCVSH+  V  F
RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRILRLFHVA 311 (SEQ ID NO:2883)
        YVP IGLS+VHRF  D  + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2884)

```

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

```

PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
          F+LIG+PGLE+A FW+ FPL S+Y+++A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
GPCR: 11  FVLIGIPGLEKAHFWVGFPLLSMYVVMFGNCIVVFIVRTERS LHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
          +STS+MPK+LA+FWF+S  I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
GPCR: 71  ALSTSTMPKILALEWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
          HA VL      +IG+ AVVRG+      PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
          NVVYGL  I+  +G+D + IS SY LI++TVL L ++  +AKAFGTCVSH+  V  F
GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRILRLFHVA 311 (SEQ ID NO:2885)
          YVP IGLS+VHRF      + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2886)

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Figure 25: Alignment with human olfactory receptor 5H12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPAMYIFLC 66
 N + +F+L G+PGL E + WL+ PLC +Y +A+ GN I+ VR E SLHEP MY FL
 HOR5: 5 NVTHPAFFLLTGIPGLESSHWSLGGPLCVMYAVALGGNTVILQAVRVEPSLHEP MY YFLS 64

PHOR: 67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FD RYV
 HOR5: 65 MLSFS DVAIS MATLPTVLR TFC LNARNITFDACLIQMFLIHFFSMMESGILLAMS FDRYV 124

PHOR: 127 AICHLR HATVLTLP RVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDV 186
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+
 HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLEPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
 M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH
 HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERL KALNTCVSH 244

PHOR: 246 VCAVFIFIVPFI GLSMVHRFSKR RDSPLPVILANIYLLVPPVLNPIVYG VKTKEIRQRIL 305
 + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKEIR+ I
 HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHLVMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309 (SEQ ID NO:2887)
 R+FH
 HOR5: 305 RMFH 308 (SEQ ID NO:2888)

Figure 1 (SEQ ID NO: 2878)

GATCAAACCTCTTTTCCATTGAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGAAGACAGTATTGAGAAAAAATTTC
TTAATAAAAAATACAACCTCAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTCAATATTATTTCTTCTTTGTTTC
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTGATC

FIG. 2A (SEQ ID NOS: 2879 & 2880)

5'	CAG	AGA	GGC	TGT	ATT	TCA	GTG	CAG	CCT	GCC	AGA	CCT	CTT	CTG	GAG	GAA	GAC	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		63		72		81		90		99		108						
	ACA	AAG	GGG	GTC	ACA	CAT	TCC	TTC	CAT	ACG	GTT	GAG	CCT	CTA	CCT	GCC	TGG	TGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		117		126		135		144		153		162						
	TGG	TCA	CAG	TTC	AGC	TTC	TTC	<u>ATG</u>	ATG	GTG	GAT	CCC	AAT	GGC	AAT	GAA	TCC	AGT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
								M	M	V	D	P	N	G	N	E	S	S
		171		180		189		198		207		216						
	GCT	ACA	TAC	TTC	ATC	CTA	ATA	GGC	CTC	CCT	GGT	TTA	GAA	GAG	GCT	CAG	TTC	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W
		225		234		243		252		261		270						
	TTG	GCC	TTC	CCA	TTG	TGC	TCC	CTC	TAC	CTT	ATT	GCT	GTG	CTA	GGT	AAC	TTG	ACA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	L	T
		279		288		297		306		315		324						
	ATC	ATC	TAC	ATT	GTG	CGG	ACT	GAG	CAC	AGC	CTG	CAT	GAG	CCC	ATG	TAT	ATA	TTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	Y	I	F
		333		342		351		360		369		378						
	CTT	TGC	ATG	CTT	TCA	GGC	ATT	GAC	ATC	CTC	ATC	TCC	ACC	TCA	TCC	ATG	CCC	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K
		387		396		405		414		423		432						
	ATG	CTG	GCC	ATC	TTC	TGG	TTC	AAT	TCC	ACT	ACC	ATC	CAG	TTT	GAT	GCT	TGT	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	L
		441		450		459		468		477		486						
	CTA	CAG	ATT	TTT	GCC	ATC	CAC	TCC	TTA	TCT	GGC	ATG	GAA	TCC	ACA	GTG	CTG	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	L
		495		504		513		522		531		540						
	GCC	ATG	GCT	TTT	GAC	CGC	TAT	GTG	GCC	ATC	TGT	CAC	CCA	CTG	CGC	CAT	GCC	ACA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	A	M	A	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T
		549		558		567		576		585		594						
	GTA	CTT	ACG	TTG	CCT	CGT	GTC	ACC	AAA	ATT	GGT	GTG	GCT	GCT	GTG	GTG	CGG	GGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G
		603		612		621		630		639		648						
	GCT	GCA	CTG	ATG	GCA	CCC	CTT	CCT	GTC	TTC	ATC	AAG	CAG	CTG	CCC	TTC	TGC	CGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R

FIG. 2B

657	666	675	684	693	702
TCC AAT ATC CTT TCC	CAT TCC TAC TGC CTA CAC	CAA GAT GTC ATG AAG CTG	GCC		
S N I L S	H S Y C L H Q D V M K L A				
711	720	729	738	747	756
TGT GAT GAT ATC CGG	GTC AAT GTC GTC TAT GGC	CTT ATC GTC ATC ATC TCC	GCC		
C D D I R V N V V Y G L I V I I S A					
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC	TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT				
I G L D S L L I S F S Y L L I L K T					
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT					
V L G L T R E A Q A K A F G T C V S					
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG					
H V C A V F I F Y V P F I G L S M V					
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC					
H R F S K R R D S P L P V I L A N I					
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG					
Y L L V P P V L N P I V Y G V K T K					
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG					
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT					
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA					
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT					
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC					
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA					



FIG. 2C

1359	1368	1377	1386	1395	1404
AAC TGC TTC	TAC TGA TGG	TTT ACA GCA	TTC TGA GAT	AAG AAT GGT	ACA TCT AGA
1413	1422	1431	1440	1449	1458
GAA CAT TTG	CCA AAG GCC	TAA GCA CGG	CAA AGG AAA	ATA AAC ACA	GAA TAT AAT
1467	1476	1485	1494	1503	1512
AAA ATG AGA	TAA TCT AGC	TTA AAA CTA	TAA CTT CCT	CTT CAG AAC	TCC CAA CCA
1521	1530	1539	1548	1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT CTT	CAA AAT GAC	TTC TAC AGA	GAA GAA ATA
1575	1584	1593	1602	1611	1620
ATT TTT CCT	CTG GAC ACT	AGC ACT TAA	GGG GAA GAT	TGG AAG TAA	AGC CTT GAA
1629	1638	1647	1656	1665	1674
AAG AGT ACA	TTT ACC TAC	GTT AAT GAA	AGT TGA CAC	ACT GTT CTG	AGA GTT TTC
1683	1692	1701	1710	1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC TAT	TTA ATT TTC	TTA TCA ACC	CTT TAA TTA
1737	1746	1755	1764	1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC ATT	GTA GCC ATG	GGA AAA TTG	ATG TTC AGT
1791	1800	1809	1818	1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT CAT	ACA AGT ATA	AAA ATT AAA	AAA AAA AAA
1845	1854	1863	1872	1881	1890
GAC TTC ATG	CCC AAT CTC	ATA TGA TGT	GGA AGA ACT	GTT AGA GAG	ACC AAC AGG
1899	1908	1917	1926	1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG TCT	TAC ATT TTC	TAG AGG AGG	TAT TTA ATT
1953	1962	1971	1980	1989	1998
TCT TCT CAC	TCA TCC AGT	GTT GTA TTT	AGG AAT TTC	CTG GCA ACA	GAA CTC ATG
2007	2016	2025	2034	2043	2052
GCT TTA ATC	CCA CTA GCT	ATT GCT TAT	TGT CCT GGT	CCA ATT GCC	AAT TAC CTG
2061	2070	2079	2088	2097	2106
TGT CTT GGA	AGA AGT GAT	TTC TAG GTT	CAC CAT TAT	GGA AGA TTC	TTA TTC AGA
2115	2124	2133	2142	2151	2160
AAG TCT GCA	TAG GGC TTA	TAG CAA GTT	ATT TAT TTT	TAA AAG TTC	CAT AGG TGA
2169	2178	2187	2196	2205	2214
TTC TGA TAG	GCA GTG AGG	TTA GGG AGC	CAC CAG TTA	TGA TGG GAA	GTA TGG AAT
2223	2232	2241	2250	2259	2268
GGC AGG TCT	TGA AGA TAA	CAT TGG CCT	TTT GAG TGT	GAC TCG TAG	CTG GAA AGT
2277	2286	2295	2304	2313	2322
GAG GGA ATC	TTC AGG ACC	ATG CTT TAT	TTG GGG CTT	TGT GCA GTA	TGG AAC AGG
2331	2340	2349	2358	2367	2376
GAC TTT GAG	ACC AGG AAA	GCA ATC TGA	CTT AGG CAT	GGG AAT CAG	GCA TTT TTG



FIG. 2D

2385	2394	2403	2412	2421	2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA					
2439	2448	2457	2466	2475	2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT					
2493	2502	2511	2520	2529	2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC					
2547	2556	2565	2574	2583	2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT					
2601	2610	2619	2628	2637	2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT					
2655	2664	2673	2682	2691	2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC					
2709	2718	2727	2736	2745	2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT					
2763	2772	2781	2790	2799	2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT					
2817	2826	2835	2844	2853	2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA					
2871	2880	2889	2898	2907	2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT					
2925	2934	2943	2952	2961	2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG					
2979	2988	2997	3006	3015	3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT					
3033	3042	3051	3060	3069	3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT					
3087	3096	3105	3114	3123	3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA					

AAA A 3'

Figure 3: Protein Sequence for 101P3A11 (*piece of SEQ ID NO: 2880*)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTITYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANTYLLVPPVLNPIVYG
VKTKEIRQRILRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

Query: 34 GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIIVLIRTSPQLHTPMYLF 93
 GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL

Sbjct: 6 GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPFI 65

Query: 94 SHLAFLDIGYSSSVTPIMLRGFLRKGTIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
 L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY

Sbjct: 66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSPFCGPNKINHFFCDYSP 213
 VAIC PL ++T ++ + + + G L FC N ++H +C +

Sbjct: 126 VAICHPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISGSIIVTVFIIALSIVYILVSILKMRSTEGRQKAFSTCTS 273
 ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S

Sbjct: 186 VMKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK---VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
 H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++

Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRDRSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQ 302

Query: 330 AMKKL 334 (SEQ ID NO: 2881)
 + +L

Sbjct: 303 RILRL 307 (SEQ ID NO: 2882)



Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
 F+LIG+PGLEEA FW FPL S+Y +A+ GN +++IVRTE SLH PMY+FLCML+ ID+
 RA1C: 11 FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERS LHAPMYLFLCMLAAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
 +STS+MPK+LA+FWF+S I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
 RA1C: 71 ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
 HA VL +IG+ A+VRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
 RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
 NVVYGL I+ +G+D + IS SY LI++ VL L ++ +AKAFGTCVSH+ V F
 RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAFL 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQRILRLFHVA 311 (SEQ ID NO: 2883)
 YVP IGLS+VHRF D + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
 RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMDVYLLLPVINPIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO: 2884)

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
 F+LIG+PGLE+A FW+ FPL S+Y++A+ GN +++IVRTE SLH PMY+FLCML+ ID+
 GPCR: 11 FVLIGIPGLEKAHFWVGFPLLSMYVVMFPGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
 +STS+MPK+LA+FWF+S I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
 GPCR: 71 ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
 HA VL +IG+ AVVRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
 GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
 NVVYGL I+ +G+D + IS SY LI++TVL L ++ +AKAFGTCVSH+ V F
 GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLPNPIVYGVTKEIRQRILRLFHVA 311 (SEQ ID NO: 2885)
 YVP IGLS+VHRF + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
 GPCR: 251 YVPLIGLSVVRHFRGNSLHPIVRVVMGDIYLLLPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO: 2886)

Figure 25: Alignment with human olfactory receptor 5H12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
 N + +F+L G+PGLE + WL+ PLC +Y +A+ GN I+ VR E SLHEPMY FL
 HOR5: 5 NVTHPAFFLLTGIPGLESSHWSLGPCLVMYAVLGGNTVILQAVRVEPSLHEPMYYFLS 64

PHOR: 67 MLSCGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FDYV
 HOR5: 65 MLFSFDVAISMATLPTVLRFTCLNARNITFDACLIQMFILHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDV 186
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+
 HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPPLFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
 M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH
 HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFIFGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRIL 305
 + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKAIR+ I
 HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309 (SEQ ID NO: 2887)
 R+FH
 HOR5: 305 RMFH 308 (SEQ ID NO: 2888)